

## **FIGURE 1**

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTACAAAAGGTGCAGGTATG  
AGCAGGTCTGAAGACTAACATTTTGTGAAGTTGTAAACAGAAAACCTGTTAGAAATGTGGTGGT  
TTCAGCAAGGCCTCAGTTTCCTTCCTTCAGCCCTTGTAAATTTGGACATCTGCTGCTTTCATATTT  
TCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTTACCTTATATCAGTGACACTGG  
TACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTAAATATTGCGGCAGTTTTATGCATTG  
CTACCATTTATGTTTCGTTATAAGCAAGTTCATGCTCTGAGTCCTGAAGAGAACGTTATCATCAAA  
TTAAACAAGGCTGGCCTTGTACTTGAATACTGAGTTGTTTAGGACTTCTATTGTGGCAAACTT  
CCAGAAAACAACCCCTTTTTGCTGCACATGTAAGTGGAGCTGTGCTTACCTTTGGTATGGGCTCAT  
TATATATGTTTGTTCAGACCATCCTTTCCCTACCAAATGCAGCCCAAAATCCATGGCAAACAAGTC  
TTCTGGATCAGACTGTTGTTGGTTATCTGGTGTGGAGTAAGTGCACCTAGCATGCTGACTTGCTC  
ATCAGTTTTGCACAGTGGCAATTTTGGGACTGATTTAGAACAGAACTCCATTGGAACCCCGAGG  
ACAAAGGTTATGTGCTTCACATGATCACTACTGCAGCAGAATGGTCTATGTCAATTTTCCTTCTTT  
GGTTTTTTCCTGACTTACATTCGTGATTTTCAGAAAATTTCTTTACGGGTGGAAGCCAATTTACA  
TGGATTAACCTCTATGACACTGCACCTTGCCCTATTAACAATGAACGAACACGGCTACTTTCCA  
GAGATATTTGATGAAAGGATAAAAATATTTCTGTAATGATTATGATTCTCAGGGATTGGGGAAAGG  
TTCACAGAAGTTGCTTATTCTTCTCTGAAATTTTCAACCACTTAATCAAGGCTGACAGTAACACT  
GATGAATGCTGATAATCAGGAAACATGAAAGAAGCCATTTGATAGATTATTCTAAAGGATATCAT  
CAAGAAGACTATTAAAAACACCTATGCCTATACTTTTTTATCTCAGAAAATAAAGTCAAAAGACT  
ATG

## **FIGURE 2**

<subunit 1 of 1, 266 aa, 1 stop

<MW: 29766, pI: 8.39, NX(S/T): 0

MWWFQQGLSFLPSALVIWTSAAFIIFSITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNIAAV  
LCIATIIYVRYKQVHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSGAVLTFG  
MGSLYMFVQTILSYQMOPKIHGKQVFWIRLLLVICWCGVSALSMLTCSSVLHSGNFGTDLEQKLHW  
NPEDKGYVLHMITTAAEWSMSFSFFGFFLTYYIRDFQKISLRVEANLHGLTLYDTAPCPINNERTR  
LLSRDI

### **Important features:**

#### **Type II transmembrane domain:**

amino acids 13-33

#### **Other Transmembrane domains:**

amino acids 54-73, 94-113, 160-180, 122-141

#### **N-myristoylation sites.**

amino acids 57-63, 95-101, 99-105, 124-130, 183-189

### FIGURE 3

CGGACGCGTGGGCGGACGCGTGGGGGAGAGCCGCGAGTCCCGGCTGCAGCACCTGGGAGAAGGCAGACC  
GTGTGAGGGGGCCTGTGGCCCCAGCGTGCTGTGGCCTCGGGGAGTGGGAAGTGGAGGCAGGAGCCTTC  
CTTACACTTCGCCATGAGTTTCCTCATCGACTCCAGCATCATGATTACCTCCCAGATACTATTTTTTG  
GATTTGGGTGGCTTTTCTTCATGCGCCAATTGTTTAAAGACTATGAGATACGTCAGTATGTTGTACAG  
GTGATCTTCTCCGTGACGTTTGCATTTTCTTGCAACCATGTTTGAGCTCATCATCTTTGAAATCTTAGG  
AGTATTGAATAGCAGCTCCCCTTATTTTCACTGGAAAATGAACCTGTGTGTAATCTGCTGATCCTGG  
TTTTTCATGGTGCCTTTTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCATAAACAACGA  
CTGCTTTTTTCTGTCTCTTATGGCTGACCTTTATGTATTTCTTCTGGAACTAGGAGATCCCTTTCC  
CATTCTCAGCCCAAAACATGGGATCTTATCCATAGAACAGCTCATCAGCCGGGTGGTGTGATTGGAG  
TGACTCTCATGGCTCTTCTTTCTGGATTGGTGCTGTCAACTGCCCATACACTTACATGTCTTACTTC  
CTCAGGAATGTGACTGACACGGATATTCTAGCCCTGGAACGGCGACTGCTGCAAACCATGGATATGAT  
CATAAGCAAAAAGAAAAGGATGGCAATGGCACGGAGAACAATGTTCCAGAAGGGGGAAGTGCATAACA  
AACCATCAGGTTTCTGGGGAATGATAAAAAGTGTACCACCTCAGCATCAGGAAGTGAAAATCTTACT  
CTTATTCAACAGGAAGTGGATGCTTTGGAAGAATTAAGCAGGCAGCTTTTCTGGAAACAGCTGATCT  
ATATGCTACCAAGGAGAGAATAGAATACTCCAAAACCTTCAAGGGGAAATATTTTAATTTTCTTGGTT  
ACTTTTTCTCTATTTACTGTGTTTGGAAAATTTTCATGGCTACCATCAATATTGTTTTTGATCGAGTT  
GGGAAAACGGATCCTGTCACAAGAGGCATTGAGATCACTGTGAATTATCTGGGAATCCAATTTGATGT  
GAAGTTTTGGTCCCAACACATTTCTTCATTCTTGTGGAATAATCATCGTCACATCCATCAGAGGAT  
TGCTGATCACTCTTACCAAGTTCTTTTATGCCATCTCTAGCAGTAAGTCTCCAATGTCATTGTCCTG  
CTATTAGCACAGATAATGGGCATGTACTTTGTCTCCTCTGTGCTGCTGATCCGAATGAGTATGCCTTT  
AGAATACCGCACCATAATCACTGAAGTCTTGGAGAACTGCAGTTCAACTTCTATCACCGTTGGTTTG  
ATGTGATCTTCCTGGTCAGCGCTCTCTCTAGCATACTCTTCCTCTATTTGGCTCACAAACAGGCACCA  
GAGAAGCAAATGGCACCTTGAACTTAAGCCTACTACAGACTGTTAGAGGCCAGTGGTTTCAAATTTA  
GATATAAGAGGGGGGAAAAATGGAACCAGGGCCTGACATTTTATAAACAAACAAAATGCTATGGTAGC  
ATTTTTACCTTCATAGCATACTCCTTCCCGTCAGGTGATACTATGACCATGAGTAGCATCAGCCAG  
AACATGAGAGGGGAGAACTCAAGACAATACTCAGCAGAGAGCATCCCGTGTGGATATGAGGCTGG  
TGTAGAGGCGGAGAGGAGCCAAGAACTAAAGGTGAAAAATACACTGGAACCTCTGGGGCAAGACATGT  
CTATGGTAGCTGAGCCAAACACGTAGGATTTCCGTTTAAAGGTTACATGGAAAAGGTTATAGCTTTG  
CCTTGAGATTGACTCATTAAATCAGAGACTGTAACAAAAAAGGGCGCGCGC  
ACTCTAGAGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTGTTTATTGCAGCTTATAATG

## **FIGURE 4**

MSFLIDSSIMITSQILFFGFGWLFFMRQLFKDYEIRQYVVQVIFSVTFAFSCTMFELIIFEILGV  
LNSSRYFHWKMNLVCVILLILVFMVPFYIGYFIVSNIRLLHKQRLLFSCLLWLTFMYFFWKLGDP  
FPILSPKHGILSIEQLISRVGIVGVTLMALLSGFGAVNCPYTYMSYFLRNVTDTDILALERLLQ  
TMDMIISKKRMAMARRTMFQKGEVHNKPSGFWGMIKSVTTSASGSENLTLIQQEVDLEELSRQ  
LFLETADLYATKERIEYSKTFKGKYFNFLGYFFSIYCVWKIFMATINIVFDRVGKTDPVTRGIEI  
TVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTKFFYAISSSKSSNVIVLLLAQIMGY  
FVSSVLLIRMSMPLEYRTIITEVLGELQFNFYHRWFDVIFLVSALSSILFLYLAHKQAPEKQMAP

### **Important features:**

#### **Signal peptide:**

amino acids 1-23

#### **Potential transmembrane domains:**

amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398,  
425-444

#### **N-glycosylation sites.**

amino acids 67-70, 180-183 and 243-246

#### **Eukaryotic cobalamin-binding proteins**

amino acids 151-160

## FIGURE 5

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGTTCC  
 AGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATCTGAGGT  
 GTTTCCTGGCTCTGAAGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACT  
 TCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGT  
 GTCATGCAGAATTATGGGATCACCCCTTGTGAGCAAAAAGGCCAACCAGCAGCTGAATTTACAG  
 AAGCTAAGGAGGCTGTAGGCTGCTGGGACTAAGTTGGCCGGCAAGGACCAAGTTGAAACAGCC  
 TTGAAAGCTAGCTTTGAACTTGCAGCTATGGCTGGGTTGGAGATGGATTCTGTTGCTATCTCTAG  
 GATTAGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTCTGATTTGGAAGGTTCCAGTGA  
 GCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCATTCCAGAA  
 ATTATCACCACCAAAGATCCCATATTCAACACTCAAACGCAACAAACAAGAATTTATTGT  
 CAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCTTACTACTCCTC  
 CTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTTGTGTACAGAAGTTTTTATG  
 GAACTAGCACCATGTCTACAGAACTGAACCATTTGTGAAAATAAAGCAGCATTCAAGAATGA  
 AGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTGCTAGTGCTTGTCTCCTCTCTTTGGTGTG  
 CAGCTGGTCTTGGATTTTGTATGTCAAAAGGTATGTGAAGGCCCTCCCTTTTACAAACAAGAA  
 CAGCAGAAGGAAATGATCGAAACCAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCCTAA  
 TGAGGAATCAAAGAACTGATAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAACTACCGTGC  
 GATGCCCTGGAAGCTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTTCTTT  
 CATGCTCCTTACCCTGCCCTGAGCTGGGAAATCAAAGGGCCAAAGAACCAAGAAGAAAGTCCA  
 CCCTTGGTTCCCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAT  
 GCCCTTCTCCTTATTGTAACCTGTCTGGATCCTATCCTCCTACCTCAAAGCTTCCCACGGCCT  
 TTCTAGCCTGGCTATGTCTTAATAATATCCCACTGGGAGAAAGGAGTTTTCGAAAGTGCAAGGAC  
 CTAAACATCTCATCAGTATCCAGTGGTAAAAAGGCCCTCCTGGCTGTCTGAGGCTAGGTGGGTTG  
 AAAGCCAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCCGCAGCTCAGACCCTTCTTCA  
 GCTCTGAAAGAGAAACACGTATCCACCTGACATGTCTTCTGAGCCCGGTAAGAGCAAAAGAAT  
 GGCAGAAAAGTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAATCTCTGTAAA  
 GCTAAAATAAAGAAATAGAACAAAGGCTGAGGATACGACAGTACACTGTGAGCAGGGACTGTAAAC  
 ACAGACAGGGTCAAAGTGTTTTCTCTGAACACATTGAGTTGGAATCACTGTTTAGAACACACACA  
 CTTACTTTTTCTGGTCTCTACCACTGCTGATATTTCTCTAGGAAATATACTTTTACAAGTAACA  
 AAAATAAAACTCTTATAAATTCTATTTTATCTGAGTTACAGAAATGATTACTAAGGAAGATT  
 ACTCAGTAATTTGTTTAAAAAGTAATAAAATTCAACAAACATTTGCTGAATAGCTACTATATGTC  
 AAGTGCTGTGCAAGGTATTACACTCTGTAATTGAATATTATTCCTCAAAAAATTGCACATAGTAG  
 AACGCTATCTGGGAAGCTATTTTTTTCAGTTTGTATTTCTAGCTTATCTACTTCCAAACTAAT  
 TTTTATTTTTGCTGAGACTAATCTTATTCATTTTCTCTAATATGGCAACCATTATAACCTTAATT  
 TATTATTAACATACCTAAGAAGTACATTGTTACCTCTATATACCAAAGCACATTTTAAAGTGCC  
 ATTAACAAATGTATCACTAGCCCTCCTTTTTCCAACAAGAAGGACTGAGAGATGCAGAAATATT  
 TGTGACAAAAAATTAAAGCATTTAGAAAACCTT

## **FIGURE 6**

MARCFSLVLLLTISIWTTRLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLG  
LSLAGKDQVETALKASFETCSYGWVGDFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYN  
SSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPAPASTSIPR  
RKKLICVTEVFMETSTMSTETEPFVENKAAFKNAAAGFGGVPTALLVLALLFFGAAAGLGFCYVK  
RYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSPSKTTVRCLEAEV

### **Signal sequence:**

amino acids 1-16

### **Transmembrane domain:**

amino acids 235-254

### **N-glycosylation site.**

amino acids 53-57, 130-134, 289-293

### **Casein kinase II phosphorylation site.**

amino acids 145-149, 214-218

### **Tyrosine kinase phosphorylation site.**

amino acids 79-88

### **N-myristoylation site.**

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

## FIGURE 7

CGCCGCGCTCCCGCACCCGCGGCCCCGCCACCGCGCGCTCCCGCATCTGCACCCGAGCCCGGC  
GGCCTCCCGGGGGAGCGAGCAGATCCAGTCCGGCCCCGAGCGCAACTCGGTCCAGTCGGGGCGG  
CGGCTGCGGGGCGCAGAGCGGAGATGAGCGGCTTGGGGCCACCCTGCTGTGCCTGCTGCTGGCGG  
CGGCGGTCCCCACGGCCCCCGCGCCCGCTCCGACGGCGACCTCGGCTCCAGTCAAGCCCCGCCCCG  
GCTCTCAGCTACCCGACAGGAGGAGGCCACCCTCAATGAGATGTTCCGCGAGGTTGAGGAACTGAT  
GGAGGACACGCAGCACAAATTGCGCAGCGCGGTGGAAGAGATGGAGGCAGAAGAAGCTGCTGCTA  
AAGCATCATCAGAAGTGAACCTGGCAAACCTTACCTCCCAGCTATCACAATGAGACCAACACAGAC  
ACGAAGGTTGGAAATAATACCATCCATGTGCACCGAGAAATTCACAAGATAACCAACAACCAGAC  
TGGACAAATGGTCTTTTCAGAGACAGTTATCACATCTGTGGGAGACGAAGAAGGCAGAAGGAGCC  
ACGAGTGCATCATCGACGAGGACTGTGGGCCCCAGCATGTACTGCCAGTTTGCCAGCTTCCAGTAC  
ACCTGCCAGCCATGCCGGGGCCAGAGGATGCTCTGCACCCGGGACAGTGAGTGTGTGGAGACCA  
GCTGTGTGTCTGGGGTCACTGCACCAAAATGGCCACCAGGGGCGAGCAATGGGACCATCTGTGACA  
ACCAGAGGGACTGCCAGCCGGGGCTGTGCTGTGCCTTCCAGAGAGGCTGCTGTTCCCTGTGTGC  
ACACCCCTGCCCGTGGAGGGCGAGCTTTGCCATGACCCGCCAGCCGGCTTCTGGACCTCATCAC  
CTGGGAGCTAGAGCCTGATGGAGCCTTGACCGATGCCCTTGTGCCAGTGGCCTCCTCTGCCAGC  
CCCACAGCCACAGCCTGGTGTATGTGTGCAAGCCGACCTTCGTGGGGAGCCGTGACCAAGATGGG  
GAGATCCTGCTGCCCAGAGAGGTCCCCGATGAGTATGAAGTTGGCAGCTTCATGGAGGAGGTGCG  
CCAGGAGCTGGAGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGCTGGGGGAGCCTGCGGCTG  
CCGCGCTGCACTGCTGGGAGGGGAAGAGATTAGATCTGGACCAGGCTGTGGGTAGATGTGCAA  
TAGAAATAGCTAATTTATTTCCCCAGGTGTGTGCTTTAGGCGTGGGCTGACCAGGCTTCTTCCCTA  
CATCTTCTTCCAGTAAGTTTCCCCTCTGGCTTGACAGCATGAGGTGTGTGCAATTTGTTTCAGT  
CCCCAGGCTGTTCTCTCAGGCTTACAGTCTGGTGCTTGGGAGAGTCAGGCAGGGTTAAACTGCA  
GGAGCAGTTTGGCCACCCTGTCCAGATTATTGGCTGCTTTGCCTCTACCAAGTTGGCAGACAGCCG  
TTTGTCTACATGGCTTTGATAATTGTTTGGGGGAGGAGATGGAACAATGTGGAGTCTCCCTC  
TGATTGGTTTTGGGGAAATGTGGAGAAGAGTGCCCTGCTTTGCAAACATCAACCTGGCAAAATG  
CAACAAATGAATTTCCACGCAGTTCTTTCCATGGGCATAGGTAAGCTGTGCCTTCAGCTGTTGC  
AGATGAAATGTTCTGTTACCCCTGCATTACATGTGTTTATTCATCCAGCAGTGTGCTCAGCTCC  
TACCTCTGTGCCAGGGCAGCATTTTCATATCCAAGATCAATTCCCTCTCTCAGCACAGCCTGGGG  
AGGGGGTCATTGTTCTCCTCGTCCATCAGGGATCTCAGAGGCTCAGAGACTGCAAGCTGCTTGCC  
CAAGTCACACAGCTAGTGAAGACCAGAGCAGTTTCATCTGGTTGTGACTCTAAGCTCAGTGCTCT  
CTCCACTACCCACACAGCCTTGGTGCCACCAAAAGTGCTCCCCAAAGGAAGGAGAATGGGAT  
TTTTCTTGAGGCATGCACATCTGGAATTAAGGTCAAACAAATCTCACATCCCTCTAAAAGTAAA  
CTACTGTTAGGAACAGCAGTGTCTCACAGTGTGGGGCAGCCGTCCTTCTAATGAAGACAATGAT  
ATTGACACTGTCCCTCTTTGGCAGTTGCATTAGTAACCTTGAAAGGTATATGACTGAGCGTAGCA  
TACAGGTTAACCTGCAGAAACAGTACTTAGGTAATTGTAGGGCGAGGATTATAAATGAAATTTGC  
AAAATCACTTAGCAGCAACTGAAGACAATTATCAACCACGTGGAGAAAATCAAACCGAGCAGGGC  
TGTGTGAAACATGGTTGTAATATGCGACTGCGAACACTGAACTCTACGCCACTCCACAAATGATG  
TTTTCAGGTGTGATGGACTGTTGCCACCATGTATTATCCAGAGTCTTAAAGTTTAAAGTTGCA  
CATGATTGTATAAGCATGCTTTCTTTGAGTTTTAAATTATGTATAAACATAAGTTGCATTTAGAA  
ATCAAGCATAAATCACTTCAACTGCAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 8**

MQRLGATLLCLLLAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQHKL  
RSAVEEMEAEEAAKASSEVNLANLPSPYHNETNTDTKVGNNTIHVHREIHKITNNQTGQMVFSE  
TVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRQGRMLCTRDECCGDQLCVWGHC  
TKMATRGSNGTICDNQRDCQPLCCAFQRGLLFPVCTPLPVEGELCHDPASRLDLITWELEPDG  
ALDRCPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEVGSFMEEVRQLELDLE  
RSLTEEMALGEPAAAAAALLGGEI

### **Signal sequence:**

amino acids 1-19

### **N-glycosylation site.**

amino acids 96-100, 106-110, 121-125, 204-208

### **Casein kinase II phosphorylation site.**

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,  
327-331

### **N-myristoylation site.**

amino acids 202-208, 217-223

### **Amidation site.**

amino acids 140-144



## FIGURE 9

CGGACGCGTGGGCGGACGCGTGGGGGCTGTGAGAAAGTGCCAATAAATACATCATGCAACCCAC  
GGCCCACCTTGTGAACTCCTCGTGCCAGGGCTGATGTGCGTCTTCCAGGGCTACTCATCCAAAG  
GCCTAATCCAACGTTCTGTCTTCAATCTGCAAATCTATGGGGCTCTTCTGGACCCCTT  
AACTGGGTACTGGCCCTGGGCCAATGCGTCCTCGCTGGAGCCTTTGCCTCCTTCTACTGGGCCTT  
CCACAAGCCCCAGGACATCCCTACCTTCCCCTTAATCTCTGCCTTCATCCGCACACTCCGTTACC  
ACACTGGGTCAATTGGCATTGGAGCCCTCATCTGACCCTTGTGCAGATAGCCCGGGTCATCTTG  
GAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCCTGTAGCCCGCTGCATCATGTGCTGTTT  
CAAGTGCTGCCTCTGGTGTCTGGAAAAATTTATCAAGTTCCTAAACCGCAATGCATACATCATGA  
TCGCCATCTACGGGAAGAATTTCTGTGTCTCAGCCAAAAATGCGTTCATGCTACTCATGCGAAAC  
ATTGTCAGGGTGGTCTGCTCGGACAAAGTACAGACCTGTGCTGTTCTTTGGGAAGCTGCTGGT  
GGTCGGAGGCGTGGGGGCTCTGTCTTCTTTTTTCTCCGGTCGCATCCCGGGGCTGGGTAAAG  
ACTTTAAGAGCCCCACCTCAACTATTACTGGCTGCCCATCATGACCTCCATCCTGGGGGCTAT  
GTCATCGCCAGCGGCTTCTTCAGCGTTTTTCGGCATGTGTGTGGACACGCTCTTCTCTGCTTCCT  
GGAAGACCTGGAGCGGAACAACGGCTCCCTGGACCGGCCCTACTACATGTCCAAGAGCCTTCTAA  
AGATTCTGGGCAAGAAGAACGAGGCGCCCCGGACAACAAGAAGAGGAAGAAGTGACAGCTCCGG  
CCCTGATCCAGGACTGCACCCACCCCAACCGTCCAGCCATCCAACCTCACTTCGCCTTACAGGT  
CTCCATTTTGTGGTAAAAAAGGTTTTAGGCCAGGCGCGTGGCTCACGCCTGTAATCCAACACT  
TTGAGAGGCTGAGGCGGGCGGATCACCTGAGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGTG  
AAACCTCCGTCTCTATTAATAAATAAAAAATTAGCCGAGAGTGGTGGCATGCACCTGTCATCCCA  
GCTACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCGGGAGGCAGAGGTTGCAGTGAGCCGA  
GATCGCGCCACTGCACTCCAACCTGGGTGACAGACTCTGTCTCCAAAACAAAACAAACAAACAA  
AAGATTTTATTAAAGATATTTTGTTAACTC

## **FIGURE 10**

RTGRTRGGCEKVPINTSCNPTAHLVNSSCPGLMCVFQGYSSKGLIQRSVFNLQIYGVLGGLFWTL  
NWVLALGQCVLAFASFYWAFHKPDIPFPLISAFIRTLRYHTGSLAFGALILTLVQIARVIL  
EYIDHKLRGVQNPVARCIMCCFKCCLWCLEKFIKFLNRNAYIMIAIYGKNFCVSAKNAFMLLMRN  
IVRVVLDKVTDLLLFFGKLLVVGGVLSFFFFSGRIPGLGKDFKSPHLNYYWLPIMTSILGAY  
VIASGFFSVFGMCVDTLFLCFLEDLERNNGSLDRPYMSKSLKILGKNEAPPDNKKRKK

### **Important features:**

#### **Transmembrane domains:**

amino acids 57-80 (type II), 110-126, 215-231, 254-274

#### **N-glycosylation sites.**

amino acids 16-20, 27-31, 289-293

#### **Hypothetical YBR002c family proteins.**

amino acids 276-288

#### **Ammonium transporters proteins.**

amino acids 204-231

#### **N-myristoylation sites.**

amino acids 60-66, 78-84

#### **Amidation site.**

amino acids 306-310

[illegible][illegible]

## **FIGURE 12**

MGACLGACSLSCASCLCGSAPCILCSCCPASRNSTVSRLIFTFFLFLGLVLSIIMLSPGVESQL  
YKLPWVCEEAGIPTVLQGHIDCGSLLGYRAVYRMCFATAAFFFFFFFTLLMLCVSSSRDPRAAIQ  
NGFWFFKFLILVGLTVGAFYIPDGSFTNIWFYFGVVGSLFILIQLVLLIDFAHSWNQRWLKAE  
ECDRAWYAGLFFFTLLFYLLSIAAVALMFMYYTEPSGCHEGKVFISLNLTFVCVVSIAAVLPKV  
QDAQPNSGLLQASVITLYTMFVTWSALSSIPEQKCNPHLPTQLGNETVVAGPEGYETQWWDAPSI  
VGLIIFLLCTLFISLRSSDHRQVNSLMQTEECPPMLDATQQQQQVAACEGRAFDNEQDGVITYSY  
SFFHFCVLVLAHLVMMTLTNWYKPGETRMISTWTAVVVKICASWAGLLLYLWTLVAPLLLRNRD  
FS

### **Signal sequence:**

amino acids 1-20

### **Transmembrane domains:**

amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,  
272-283, 324-340, 391-406, 428-444

## FIGURE 13

CGGGCCAGCCTGGGGCGGCCGGCCAGGAACCACCCGTTAAGGTGTCTTCTTTAGGGATGGTGA  
GGTTGGA AAAAGACTCCTGTAACCCCTCCTCCAGGATGAACCACCTGCCAGAAGACATGGAGAACG  
CTCTCACC GGGAGCCAGAGCTCCCATGCTTCTCTGCGCAATATCCATTCCATCAACCCACACAA  
CTCATGGCCAGGATTGAGTCCTATGAAGGAAGGGAAGAAAGGCATATCTGATGTCAGGAGGAC  
TTTCTGTTTGTGTTGTACCTTTGACCTCTTATTCTGTAACATTACTGTGGATAATAGAGTTAAATG  
TGAATGGAGGCATTGAGAACACATTAGAGAAGGAGGTGATGCAGTATGACTACTATTCTTCATAT  
TTTGATATATTTCTTCTGGCAGTTTTTCGATTTAAAGTGTTAATACTTGCATATGCTGTGTGCAG  
ACTGCGCCATTGGTGGGCAATAGCGTTGACAACGGCAGTGACCAGTGCCTTTTTACTAGCAAAAAG  
TGATCCTTTTCGAAGCTTTTCTCTCAAGGGGCTTTTGGCTATGTGCTGCCCATCATTTTCATTTC  
CTTGCCCTGGATTGAGACGTGGTTCTGGATTTCAAAGTGTTACCTCAAGAAGCAGAAGAAGAAAA  
CAGACTCCTGATAGTTTCCAGGATGCTTCAGAGAGGGCAGCACTTATACCTGGTGGTCTTTCTGATG  
GTCAGTTTTATTCCCCTCCTGAATCCGAAGCAGGATCTGAAGAAGCTGAAGAAAAACAGGACAGT  
GAGAAACCACTTTTAGAACTATGAGTACTACTTTTGTAAATGTGAAAAACCTCACAGAAAGTC  
ATCGAGGCAAAAAGAGGCAGGCAGTGGAGTCTCCCTGTCGACAGTAAAGTTGAAATGGTGACGTC  
CACTGCTGGCTTTATTGAACAGCTAATAAAGATTTATTTATTGTAATACCTCACAAACGTTGTAC  
CATATCCATGCACATTTAGTTGCCTGCCTGTGGCTGGTAAGGTAATGTCATGATTCATCCTCTCT  
TCAGTGAGACTGAGCCTGATGTGTTAACAATAGGTGAAGAAAGTCTTGTGCTGTATTCTTAATC  
AAAAGACTTAATATATTGAAGTAACACTTTTTTAGTAAGCAAGATACCTTTTTATTCAATTCAC  
AGAATGGAATTTTTTTGTTTCATGTCTCAGATTTATTTTGTATTTCTTTTTTAACACTCTACATT  
TCCCTTGTTTTTTAACTCATGCACATGTGCTCTTTGTACAGTTTTAAAAAGTGAATAAAATCTG  
ACATGTCAATGTGGCTAGTTTTATTTTTCTTGTGTTTGCATTATGTGTATGGCCTGAAGTGTGGA  
CTTGCAAAAGGGGAAGAAAGGAATTGCGAATACATGTAAATGTCACCAGACATTTGTATTATTT  
TTATCATGAAATCATGTTTTTCTCTGATTGTTCTGAAATGTTCTAAATACTCTTATTTTGAATGC  
ACAAAATGACTTAAACCATTATATCATGTTTCCTTTGCGTTCAGCCAATTTCAATTAAAATGAA  
CTAAATTAAAA

## **FIGURE 14**

MNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVTFDLLF  
VTLLWIIELNVNGGIENTLEKEVMQYDYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAIALTT  
AVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLDFKVLFPQEAEENRLLIVQDASER  
AALIPGGLSDGQFYSPPESEAGSEEAEEKQDSEKPLLEL

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-20

#### **Transmembrane domains:**

amino acids 54-72, 100-118, 130-144, 146-166

#### **N-myristoylation sites.**

amino acids 14-20, 78-84, 79-85, 202-208, 217-223

## FIGURE 15

ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCCGACCCGCCAGGAAAGACTGAGG  
 CCGCGGCCTGCCCCGCGCGCTCCCTGCGCCGCGCGCCTCCCGGGACAGAAGATGCTGCTCCAG  
 GGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCTGGGGCCTGGGGTGACAGGCTGCCCAT  
 CCGGCTGCCAGTGCAGCCAGCCACAGACAGTCTTCTGCACTGCCCCGCCAGGGGACCACGGTGCCC  
 CGAGACGTGCCACCCGACACGGTGGGGCTGTACGTCTTTGAGAACGGCATCACCATGCTCGACGC  
 AGGCAGCTTTGCCGCGCTGCCGGGCTGCAGCTCCTGGACCTGTCACAGAACCAGATCGCCAGCC  
 TGCCAGCGGGGTCTTCCAGCCACTCGCCAACCTCAGCAACCTGGACCTGACGGCCAACAGGCTG  
 CATGAAATCACCAATGAGACCTTCCGTGGCCTGCGGCGCTCGAGCGCCTCTACCTGGGCAAGAA  
 CCGCATCCGCCACATCCAGCCTGGTGCCTTCGACACGCTCGACCGCCTCCTGGAGCTCAAGCTGC  
 AGGACAACGAGCTGCGGGCACTGCCCCGCTGCGCCTGCCCCGCTGTGCTGCTGGACCTCAGC  
 CACAACAGCCTCCTGGCCCTGGAGCCCGGCATCCTGGACACTGCCAACGTGGAGGCGCTGCGGCT  
 GGCTGGTCTGGGGCTGCAGCAGCTGGACGAGGGGCTCTTCAGCCGCTTGCGCAACCTCCACGACC  
 TGGATGTGTCCGACAACCAGCTGGAGCGAGTGCCACCTGTGATCCGAGGCGCTCCGGGCGCTGACG  
 CGCCTGCGGCTGGCCGGCAACCCCGCATTGCCAGCTGCGGCGCGAGGACCTGGCCGGCCTGGC  
 TGCCCTGCAGGAGCTGGATGTGAGCAACCTAAGCCTGCAGGCCCTGCGTGGCGACCTCTCGGGCC  
 TCTTCCCCCGCTGCGGCTGCTGGCAGCTGCCCCGAACCCCTTCAACTGCGTGTGCCCCCTGAGC  
 TGGTTTGGCCCCCTGGGTGCGCGAGAGCCACGTACACTGGCCAGCCCTGAGGAGACGCGCTGCCA  
 CTTCCCGCCCCAAGAAGCTGGCCGGCTGCTCCTGGAGCTTGACTACGCCACTTTGGCTGCCAG  
 CCACCACCACCACAGCCACAGTGGCCACCACGAGGCCCGTGGTGGGGAGCCCCACAGCCTTGTCT  
 TCTAGCTTGGCTCCTACCTGGCTTAGCCCCACAGCGCCGCGCACTGAGGCCCCAGCCCGCCCTC  
 CACTGCCCCACCGACTGTAGGGCTGTCCCCAGCCCCAGGACTGCCACCGTCCACCTGCCTCA  
 ATGGGGGCACATGCCACCTGGGGACACGGCACCACTGGCGTGCTTGTGCCCCGAAGGCTTCAGC  
 GGCTGTACTGTGAGAGCCAGATGGGGCAGGGGACACGGCCAGCCCTACACAGTCACGCCGAG  
 GCCACCACGGTCCCTGACCCTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGCGTGGGGCTGC  
 AGCGCTACCTCCAGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCG  
 GGCCCTGATAAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTGAGTACACGGTCACCCA  
 GCTGCGGCCCCAACGCCACTTACTCCGTCTGTGTCATGCCTTTGGGGCGCGGGCGGGTGCCGAGG  
 GCGAGGAGGCTGCGGGGAGGCCCATACACCCCGCCGCTCCACTCCAACCACGCCCCAGTCACC  
 CAGGCCCGCGAGGGCAACCTGCCGCTCCTCATTGCGCCCGCCCTGGCCGCGGTGCTCCTGGCCGC  
 GCTGGCTGCGGTGGGGGCAGCCTACTGTGTGCGCGGGGGCGGCCATGGCAGCAGCGGCTCAGG  
 ACAAGGGCAGGTGGGGCCAGGGGCTGGGCCCTGGAAGTGGAGGGAGTGAAGGTCCCTTTGGAG  
 CCAGGCCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTGCCAGCGGGTCTGAGTGTGAGGTGCC  
 ACTCATGGGCTTCCCAGGGCCTGGCCTCCAGTCACCCCTCCACGCAAAGCCCTACATCTAAGCCA  
 GAGAGAGACAGGGCAGCTGGGGCCGGGCTCTCAGCCAGTGAGATGGCCAGCCCCCTCCTGCTGCC  
 ACACCACGTAAGTTCTCAGTCCCAACCTCGGGGATGTGTGACAGAGGGCTGTGTGACCACAGCT  
 GGGCCCTGTTCCCTCTGGACCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCC  
 CTAACGTCCCCAGAACCAGTGCCTATGAGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTC  
 CCTGGGCACGGCGGGCCTGCCATGTGCTGGTAACGCATGCCTGGGTCTGCTGGGCTCTCCAC  
 TCCAGGCGGACCCTGGGGGCCAGTGAAGGAAGCTCCCGGAAAGAGCAGAGGGAGAGCGGGTAGGC  
 GGCTGTGTGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAGAACTGGAAAGGAAGATGC  
 TTTAGGAACATGTTTTGCTTTTTTAAATATATATATTTATAAGAGATCCTTTCCCATTTATTCT  
 GGGAGATGTTTTCAAACCTCAGAGACAAGGACTTTGGTTTTTTGTAAGACAAACGATGATATGAA  
 GGCCTTTTGTAAAGAAAAATAAAGATGAAGTGTGAAA

## **FIGURE 16**

MCSRVP LLLPL LLL LLLALGPGVQGCPSGCQCSQPQT V FCTARQGT TVPRDVPPDTVGLYVFENGIT  
MLDAGS FAGLPGLQLLDLSQNQIASLPSGVFQPLANLSNLDLTANRLHEITNETFRGLRRLERLY  
LGKNRIRHIQPGAFDTLDRLLELKLQDNELRALPPLRLPRLLLLDL SHNSLLALEPGILD TANVE  
ALRLAGLGLQQLDEGLFSRLRNLHDLVDSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQLRPEDL  
AGLAALQELDVSNLSLQALPGDLSGLFPRLRLAAARNPFNCVCPLSWFGPWVRESHVTLASPEE  
TRCHFPPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSLAPTWLSPTAPATEAP  
SPPSTAPPTVGPVPQPDCCPSTCLNGGTCHLGTRHHLACLCPEGFTGLYCESQMGQTRPSPTP  
VTPRPRS LTLGIEPVSPTSLRVGLQRYLQGSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEY  
TVTQLRPNATYSVCVMP L GPRVPEGEEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAV  
LLAALAAVGAAYCVRGRAMAAAAQDKGQVGPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSE  
CEVPLMGFP GPGLSPLHAKPYI

### **Important features:**

#### **Signal peptide:**

amino acids 1-23

#### **Transmembrane domain:**

amino acids 579-599

#### **EGF-like domain cysteine pattern signature.**

amino acids 430-442

#### **Leucine zipper pattern.**

amino acids 197-219, 269-291

#### **N-glycosylation sites.**

amino acids 101-105, 117-121, 273-277, 500-504, 528-532

#### **Tyrosine kinase phosphorylation sites.**

amino acids 124-131, 337-345

#### **N-myristoylation sites.**

amino acids 23-29, 27-33, 70-76, 142-148, 187-193, 348-354,  
594-600, 640-646



## FIGURE 17

GCAGCGGCGAGGCGGCGGTGGTGGCTGAGTCCGTGGTGGCAGAGGCGAAGGCGACAGCTCATGCG  
GGTCCGGATAGGGCTGACGCTGCTGCTGTGTGCGGTGCTGCTGAGCTTGGCCTCGGCGTCTCGG  
ATGAAGAAGGCAGCCAGGATGAATCCTTAGATTCCAAGACTACTTTGACATCAGATGAGTCAGTA  
AAGGACCATACTACTGCAGGCAGAGTAGTTGCTGGTCAAATATTTCTTGATTGAGAAGAATCTGA  
ATTAGAATCCTCTATTCAAGAAGAGGAAGACAGCCTCAAGAGCCAAGAGGGGAAAGTGTCACAG  
AAGATATCAGCTTTCTAGAGTCTCCAAATCCAGAAAACAAGGACTATGAAGAGCCAAAGAAAGTA  
CGGAAACCAGCTTTGACCGCCATTGAAGGCACAGCACATGGGGAGCCCTGCCACTTCCCTTTTCT  
TTTCTAGATAAGGAGTATGATGAATGTACATCAGATGGGAGGGAAGATGGCAGACTGTGGTGTG  
CTACAACCTATGACTACAAAGCAGATGAAAAGTGGGGCTTTTGTGAACTGAAGAAGAGGCTGCT  
AAGAGACGGCAGATGCAGGAAGCAGAAATGATGTATCAAACCTGGAATGAAAATCCTTAATGGAAG  
CAATAAGAAAAGCCAAAAAAGAGAAGCATATCGGTATCTCCAAAAGGCAGCAAGCATGAACCATA  
CCAAAGCCCTGGAGAGAGTGTCTATGCTCTTTTATTTGGTGATTACTTGCCACAGAATATCCAG  
GCAGCGAGAGAGATGTTTGAGAAGCTGACTGAGGAAGGCTCTCCCAAGGGACAGACTGCTCTGG  
CTTTCTGTATGCCTCTGGACTTGGTGTAAATCAAGTCAGGCAAAGGCTCTTGATATTATACAT  
TTGGAGCTCTTGGGGCAATCTAATAGCCCATGTTTGGTAAGTAGACTTTAGTGGAAGGCT  
AATAATATTAACATCAGAAGAATTTGTGGTTTATAGCGGCCACAACTTTTTCAGCTTTCATGATC  
CAGATTTGCTTGTTAAGACCAAATATTCAGTTGAACCTCCTTCAAATTCTTGTTAATGGATAT  
AACACATGGAATCTACATGTAAATGAAAGTTGGTGGAGTCCACAATTTTTCTTTAAATGATTAG  
TTTGGCTGATTGCCCCATAAAAAGAGAGATCTGATAAATGGCTCTTTTAAATTTTCTCTGAGTTG  
GAATTGTCAGAATCATTTTTTACATTAGATTATCATAATTTTAAATTTTCTTTAGTTTTTCA  
AAATTTTGTAATGGTGGCTATAGAAAACAACATGAAATATTATACAATATTTTGCAACAATGC  
CCTAAGAATTGTTAAATTCATGGAGTTATTTGTGCAGAAATGACTCCAGAGAGCTCTACTTTCTG  
TTTTTTACTTTTCATGATTGGCTGTCTTCCCATTTATTCTGGTCATTTATTGCTAGTGACACTGT  
GCCTGCTTCCAGTAGTCTCATTTTCCCTATTTGCTAATTTGTTACTTTTTCTTTGCTAATTTGG  
AAGATTAACATCATTTTTAATAAAATTATGTCTAAGATTAAAAAAAAAAAAAAAAAAAAAAAAA  
AAA

## **FIGURE 18**

MRVRIGLTLLLCVLLSLASASSDEEGSQDESLSKTTLTSDSVKDHTTAGRVVAGQIFLDSESEL  
ESSIQEEEDSLKSQEGESVTEDISFLESPNPNKDYEEPKKVRKPALTAIEGTAHGEPCHFPLFLDK  
EYDECTSDGREDGRLWCATTYDYKADEKWGFCETEEEEAAKRRMQEAEMMYQTGMKILNGSNKKSQKR  
EAYRYLQKAASMNHTKALERSYALLFGDYLPQNIQAAREMFELTEEGSPKGQTALGFLYASGLGVN  
SSQAKALVYYTFGALGGNLIHMLVLSRL

### **Important features:**

#### **Signal peptide:**

amino acids 1-21

#### **N-glycosylation sites.**

amino acids 195-199, 217-221, 272-276

#### **Tyrosine kinase phosphorylation site.**

amino acids 220-228

#### **N-myristoylation sites.**

amino acids 120-126, 253-259, 268-274, 270-274, 285-291, 289-295

#### **Glycosaminoglycan attachment site.**

amino acids 267-271

#### **Microbodies C-terminal targeting signal.**

amino acids 299-303

#### **Type II fibronectin collagen-binding domain protein.**

amino acids 127-169

#### **Fructose-bisphosphate aldolase class-II protein.**

amino acids 101-119

## FIGURE 19

AATTCAGATTTTAAGCCCATTCTGCAGTGGAAATTCATGAACTAGCAAGAGGACACCATCTTCTT  
GTATTATACAAGAAAGGAGTGTACCTATCACACACAGGGGGAAAAATGCTCTTTTGGGTGCTAGG  
CCTCCTAATCCTCTGTGGTTTTCTGTGGACTCGTAAAGGAAAACATAAGATTGAAGACATCACTG  
ATAAGTACATTTTATCACTGGATGTGACTCGGGCTTTGGAACTTGGCAGCCAGAACTTTTGAT  
AAAAAGGGATTTTATGTAATCGCTGCCTGTCTGACTGAATCAGGATCAACAGCTTTAAAGGCAGA  
AACCTCAGAGAGACTTCGTACTGTGCTTCTGGATGTGACCGACCCAGAGAATGTCAAGAGGACTG  
CCCAGTGGGTGAAGAACCAAGTTGGGGAGAAAGGTCTCTGGGGTCTGATCAATAATGCTGGTGT  
CCCCGGCTGCTGGCTCCCACTGACTGGCTGACACTAGAGGACTACAGAGAACCTATTGAAGTGAA  
CCTGTTTGGACTCATCAGTGTGACACTAAATATGCTTCCTTTGGTCAAGAAAGCTCAAGGGAGAG  
TTATTAATGTCTCCAGTGTGGAGGTGCGCTTGCAATCGTTGGAGGGGGCTATACTCCATCCAAA  
TATGCAGTGGAAAGGTTTCAATGACAGCTTAAGACGGGACATGAAAGCTTTTGGTGTGCACGTCTC  
ATGCATTGAACCAAGGATTGTTCAAAACAACTTGGCAGATCCAGTAAAGGTAATTGAAAAAAAC  
TCGCCATTTGGGAGCAGCTGTCTCCAGACATCAAACAACAATATGGAGAAGGTTACATTGAAAAA  
AGTCTAGACAACTGAAAGGAATAAATCCTATGTGAACATGGACCTCTCTCCGGTGGTAGAGTG  
CATGGACCACGCTCTAACAAGTCTCTTCCCTAAGACTCATTATGCCGCTGGAAAAGATGCCAAAA  
TTTTCTGGATACCTCTGTCTCACATGCCAGCAGCTTTGCAAGACTTTTATTGTTGAAACAGAAA  
GCAGAGCTGGCTAATCCAAGGCAGTGTGACTCAGCTAACCACAAATGTCTCCTCCAGGCTATGA  
AATTGGCCGATTTCAAGAACACATCTCCTTTTCAACCCCATTCCTTATCTGCTCCAACCTGGACT  
CATTTAGATCGTGCTTATTTGGATTGCAAAAGGGAGTCCCACCATCGCTGGTGGTATCCCAGGGT  
CCCTGCTCAAGTTTTCTTTGAAAAGGAGGGCTGGAATGGTACATCACATAGGCAAGTCCTGCCCT  
GIATTTAGGCTTTGCCTGCTTGGTGTGATGTAAGGGAAATTGAAAGACTTGCCCATTCAAATGA  
TCTTTACCGTGGCCTGCCCCATGCTTATGGTCCCCAGCATTACAGTAACTTGTGAATGTTAAGT  
ATCATCTCTTATCTAAATATTAAAAGATAAGTCAACCCAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAA

## **FIGURE 20**

MLFWVLGLLILCGFLWTRKGLKIEDITDKYIFITGCDSGFGNLAARTFDKKGFHVIAACLTESG  
STALKAETSERLRTVLLDVTDPENVKRTAQWVKNOVGEKGLWGLINNAGVPGVLAPTDWLTLEDY  
REPIEVNLFGLISVTNLNMLPLVKKAAQGRVINVSSVGGRLAIVGGGYTPSKYAVEGFNDSLRRDMK  
AFGVHVSCLIEPGLFKTNLADPVKVKIEKKLAIWEQLSPDIKQQYGEGYIEKSLDKLKGKNSYVNMD  
LSPVVECMDHALTSLFPKTHYAAGKDAKIFWIPLSHMPAALQDFLLLKQKAELANPKAV

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-17

#### **Transmembrane domain:**

amino acids 136-152

#### **N-glycosylation sites.**

amino acids 161-163, 187-190 and 253-256

#### **Glycosaminoglycan attachment site.**

amino acids 39-42

#### **N-myristoylation sites.**

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

## FIGURE 21

CTGAGGCGGCGGTAGCAATGGAGGGGGAGAGTACGTGCGGCGGTGCTCTCGGGCTTTGTGCTCGGCG  
CACTCGCTTTCCAGCACCTCAACACGGACTCGGACACGGAAGGTTTTCTTCTTGGGGAAGTAAAA  
GGTGAAGCCAAGAACAGCATTACTGATTCCCAAATGGATGATGTTGAAGTTGTTTATACAATTGA  
CATTAGAAATATATTCCATGCTATCAGCTTTTTAGCTTTTATAATTCTTCAGGCGAAGTAAATG  
AGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAAGAATGTGGTAGGTTGGTACAAATTCGGT  
CGTCATTACAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAAAACTTCAGGAGCATT  
TTCAAACCAAGACCTTGTTTTCTGCTATTAACACCAAGTATAATAACAGAAAGCTGCTCTACTC  
ATCGACTGGAACATTCCCTTATATAAACCTCAAAAAGGACTTTTTTCACAGGGTACCTTTAGTGGTT  
GCCAATCTGGGCATGTCTGAACAACTGGGTATATAAACTGTATCAGGTTCTGTATGTCCACTGG  
TTTTAGCCGAGCAGTACAAACACACAGCTCTAAATTTTTGAAGAAGATGGATCCTTAAAGGAGG  
TACATAAGATAAAATGAAATGTATGCTTCATTACAAGAGGAATTAAAGAGTATATGCAAAAAAGTG  
GAAGACAGTGAACAAGCAGTAGATAAACTAGTAAAGGATGTAAACAGATTAAAACGAGAAATTGA  
GAAAAGGAGAGGAGCACAGATTGAGGAGCAAGAGAGAAGAACATCCAAAAGACCCTCAGGAGA  
ACATTTTTCTTTGTCAGGCATTACGGACCTTTTTTCCAAATCTGAATTTCTTCATTCATGTGTT  
ATGTCTTTAAAAAATAGACATGTTTCTAAAAGTAGCTGTAACACCAACCACATCTCGATGTAGT  
AGACAATCTGACCTTAATGGTAGAACACACTGACATTCCTGAAGCTAGTCCAGCTAGTACACCAC  
AAATCATTAAAGCATAAAGCCTTAGACTTAGATGACAGATGGCAATTCAAGAGATCTCGGTTGTTA  
GATACACAAGACAAACGATCTAAAGCAAATACTGGTAGTAGTAACCAAGATAAAGCATCCAAAT  
GAGCAGCCCAGAAACAGATGAAGAAATTGAAAAGATGAAGGGTTTTGGTGAATATTCACGGTCTC  
CTACATTTTGAATCCTTTTAACCTTACAAGGAGATTTTTTTATTTGGCTGATGGGTAAAGCCAAAC  
ATTTCTATTGTTTTTACTATGTTGAGCTACTTGCAGTAAGTTCATTTGTTTTTACTATGTTTACC  
TGTTTGAGTAATACACAGATAACTCTTAGTGCATTTACTTCACAAAGTACTTTTTCAAACATCA  
GATGCTTTTATTTCCAAACCTTTTTTTCACCTTTCACTAAGTTGTTGAGGGGAAGGCTTACACAG  
ACACATTCTTTAGAATTGGAAGAGTGAGACCAGGCACAGTGGCTCACACCTGTAATCCAGCACT  
TAGGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCCTGGGCAACGTATT  
GAGACCATGTCTATTAAAAAATAAAATGGAAGCAAGAATAGCCTTATTTTCAAATATGGAAA  
GAAATTTATATGAAAATTTATCTGAGTCATTAATTTCTCCTTAAGTGATACTTTTTTAGAAGTA  
CATTATGGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCAATAAATTTGCAAAACATCATCT  
AAAATTTAAAAA

## **FIGURE 22**

MEGESTSAVLSGFVLGALAFQHLNTDSDEGFLLGGEVKGEAKNSITDSQMDDVEVVYTTIDIQKYI  
PCYQLFSFYNSSGEVNEQALKKILSNVKKNVVGWYKFRRHSDQIMTFRERLLHKNLQEHFSNQDL  
VFLLLTPSIITESCSTHRLEHSLYKPQKGLFHRVPLVVANLGMSEQLGYKTVSGSCMSTGFSRAV  
QTHSSKFFEEEDGSLKEVHKINEMYASLQEELKSICKKVEDSEQAVDKLVKDVNRLKREIEKRRGA  
QIQAAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKNRHVSKSSCNYNHHLDVVDNLTL  
MVEHTDIPEASPASTPQIIKHKALDLDLRWQFKRSRLDQTQDKRSKANTGSSNQDKASKMSSPET  
DEEIEKMKGFGEYSRSPTF

### **Important features:**

#### **Signal peptide:**

amino acids 1-19

#### **N-glycosylation sites.**

amino acids 75-79, 322-326

#### **N-myristoylation site.**

amino acids 184-154

#### **Growth factor and cytokines receptors family.**

amino acids 134-150

## FIGURE 23

GGCACAGCCGCGCGGGGAGGGCAGAGTCAGCCGAGCCGAGTCCAGCCGACGAGCGGACCAGCGCAGGGCAGCCCAA  
GCAGCGCGCAGCGAACGCCCGCCGCCGCCACACCTCTGCGGTCCCCGCGGCGCCTGCCACCTTCCCTCTCCCC  
GCGTCCCCGCTCGCCGGCCAGTCAGCTTGCCTGGGTTGCTGCCCCGCGAAACCCGAGGTACCAGCCCGCGCTCT  
GCTTCCCTGGGCGCGCGCGCTCCAGCCCTCTTCTCCCTGGCCGCGCCTGGCACCAGGGGACCCTTGCTGA  
CGCGAGGCCAGCTCTACTTTTGGCCCCGCTCTCTCCGCTGCTCGCTCTTCCACCACTCCAACCTCTCTCCC  
TCCAGCTCCACTCGTAGTCCCCGACTCCGCCAGCCCTCGGCCGCTGCCGTAGCGCGCTTCCCGTCCGGTCCCAA  
GGTGGGAACGCGTCCGCCCCGGCCCGCACCATGGCACGGTTGCGCTTGGCCGCGCTTCTCTGCACCCTGGCAGTGCTC  
AGCGCGCGCTGCTGGCTGCCGAGCTCAAGTCGAAAAGTTGCTCGGAAGTGCAGCTCTTTACGTGTCCAAAGCTTC  
AACAGAACGATGCCCCCTCCACGAGATCAACGGTGATCATTGAAGATCTGTCCCAGGGTTCTACCTGCTGCTCT  
CAAGAGATGGAGGAGAAGTACAGCTGCAAAGTAAAGATGATTTCAAAAGTGTGGTCAGCGAACAGTGCAATCATTTG  
CAAGTGTCTTTGCTTACGTTACAAGAAGTTTGATGAATCTTCAAAGAAGTACTTGAAGATGCAGAGAAATCCCTG  
AATGATATGTTTGTGAAGACATATGGCCATTTATACATGCAAAATCTGAGCTATTTAAAGATCTCTTCGTAGAGTTG  
AAACGTTACTACGTGGTGGGAAATGTGAACCTGGAAGAAATGCTAAATGACTTCTGGGCTCGCCTCTGGAGCGGATG  
TTCCGCTGGTGAAGTCCAGTACCACCTTACAGATGAGTATCTGGAATGTGTGAGCAAGTATACGGAGCAGCTGAAG  
CCCTTCGGAGATGCCCTCGCAAATTGAAGTCCAGGTTACTCGTGCTTTTGTAGCAGCCGTAATTTGCTCAAGGC  
TTAGCGGTTGGCGGAGATGCTGTGAGCAAGGTCCTCCGTGTAACCCACAGCCAGTGTACCCATGCCCTGTTGAAG  
ATGATCTACTGCTCCCACTGCCGGGCTCTCGTGACTGTGAAGCATGTTACAAGTACTGCTCAAACATCATGAGAGGC  
TGTTTGGCCAACCAAGGGGATCTCGATTTTGAATGGAACAATTTATAGATGCTATGCTGATGGTGGCAGAGAGGCTA  
GAGGGTCTTTCAACATTGAATCGGTCTGATGATGCCATCGATGTGAAGATTTCTGATGCTATATGAACATGCAGGAT  
AATAGTGTCAAGTGTCTCAGAAGGTTTTCAGGGATGTGGACCCCCAAGCCCTCCAGCTGGACGAATTTCTCGT  
TCCATCTCTGAAAGTGCCTTCAGTGTCTGCTTACAGCACATCACCCGAGGAACGCCAACACAGCAGCTGGCACT  
AGTTTGGACCGACTGGTACTGATGTCAAGGAGAACTGAAACAGGCCAAGAAATCTGGTCTCCCTTCCGAGCAAC  
GTTTGCACGATGAGAGGATGGCTGCAGGAAACGGCAATGAGGATGACTGTTGGAATGGGAAAGGCAAAAGCAGGTAC  
CTGTTTGCAGTGACAGGAAATGGATTAGCCAACAGGGCAACAACCCAGAGGTCCAGGTTGACACCAGCAACACAGAC  
ATACTGATCCTTCGTCAAATCATGGCTCTTCGAGTGATGACCAGCAAGATGAAGAATGCATACAATGGGAACGACGTG  
GACTTCTTTGATATCAGTGATGAAAGTAGTGGAGAAGGAAGTGAAGTGGCTGTGAGTATCAGCAGTGCCCTTCAGAG  
TTTGACTACAATGCCACTGACCATGCTGGGAAGAGTGCCAAATGAGAAAGCCGACAGTGCTGGTGTCCGTCTGGGGCA  
CAGGCCCTACCTCCTCACTGTCTTCTGCATCTTGTCTGTTATGCAGAGAGAGTGAGATTAATTCTCAAACCTCTGAG  
AAAAAGTGTTCATCAAAAAGTTAAAGGCACCAAGTTATCACTTTTCTACCATCCTAGTGACTTGTCTTTTAAATGAA  
TGGACAACAATGTACAGTTTTTACTATGTGGCCACTGGTTTAAAGAGTGTGACTTTGTTTTCTCATTGAGTTTGGG  
AGGAAAAGGAGCTGTGCATTGAGTTGGTCTCTGCTCCCCAAACCATGTTAAACGTGGCTAACAGTGTAGGTACAGAA  
CTATAGTTAGTTGTGCATTTGTGATTTTATCACTCTATTATTTGTTGTATGTTTTTCTCATTTCGTTTGTGGGTT  
TTTTTTTCCAACGTGTGATCTCGCCTGTTTCTTACAAGCAAACAGGGTCCCTTCTGGCACGTAACATGTACGTATT  
TCTGAAATATTAAATAGCTGTACAGAAGCAGGTTTTATTTATCATGTTATCTTATTAAGAAAAAGCCCCAAAAGC

## **FIGURE 24**

MARFGLPALLCTLAVLSAALLAAELKSKSCSEVRRLYVSKGFNKNDAPLHEINGDHLKICPQGST  
CCSQEMEKEYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSINDMFVKTYGH  
LYMQNSELFKDLFVELKRYVVGNNLEMLNDFWARLLERMFRLVNSQYHFTDEYLECVSKYTE  
QLKPFQDVPRKLKLQVTRAFVAARTFAQGLAVAGDVVSKVSVVNPTAQCTHALLKMIYCSHCRGL  
VTVKPCYNYCSNIMRGCLANQGDLD FEWNNFIDAMLMVAERLEGPFNIESVMDPIDVKISDAIMN  
MQDNSVQVSQKVFQCGPPKPLPAGRISRISSESASFARFRPHHPEERPTTAAGTSLDRLVTDVK  
EKLKQAKKFWSSLPSNVCNDERMAAGNGNEDDCWNGKGKSRYLFAVTGNGLANQGNNPEVQVDT  
KPDILILRQIMALRVMTSKMKNAYNGNDVDFDISDESSGEGSGSGCEYQQCPSEFDYNATDHAG  
KSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

### **Important features:**

#### **Signal peptide:**

amino acids 1-22

#### **ATP/GTP-binding site motif A (P-loop).**

amino acids 515-524

#### **N-glycosylation site.**

amino acids 514-518

#### **Glycosaminoglycan attachment sites.**

amino acids 494-498, 498-502

#### **N-myristoylation sites.**

amino acids 63-69, 224-230, 276-282, 438-444, 497-503, 531-537

#### **Glypicans proteins.**

amino acids 54-75, 105-157, 238-280, 309-346, 423-460, 468-506



## FIGURE 25

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCTGAC  
CTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTCTTCAAGCAACT  
TACAGCTGCACCGACAGTTGCGATGAAAGTTCTAATCTCTTCCCTCCTCCTGTTGCTGCCACTAA  
TGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTGCCCAGAGGCCACAGGGACCGAGGC  
CAGGCTTCTAGGAGATGGCTCCAGGAAGGCGGCCAAGAATGTGAGTGCAAAGATTGGTTCCTGAG  
AGCCCCGAGAAGAAAATTTCATGACAGTGTCTGGGCTGCCAAAGAAGCAGTGCCCCCTGTGATCATT  
TCAAGGGCAATGTGAAGAAAACAAGACACCAAAGGCACCACAGAAAGCCAAACAAGCATTCCAGA  
GCCTGCCAGCAATTTCTCAAACAATGTCAGCTAAGAAGCTTTGCTCTGCCTTTGTAGGAGCTCTG  
AGCGCCCACTCTTCCAATTAAACATTCTCAGCCAAGAAGACAGTGAGCACACCTACCAGACACTC  
TTCTTCTCCCACCTCACTCTCCCCTGTACCCACCCCTAAATCATTCCAGTGCTCTCAAAAAGCA  
TGTTTTTCAAGATCATTTTGTGTTGCTCTCTCTAGTGTCTTCTCTCTCGTCAGTCTTAGCCT  
GTGCCCTCCCCCTTACCCAGGCTTAGGCTTAATTACCTGAAAGATTCCAGGAAACTGTAGCTTCCT  
AGCTAGTGTCAATTAACCTTAAATGCAATCAGGAAAGTAGCAAACAGAAGTCAATAAATATTTTT  
AAATGTCAAAAAAAAAAAAAAAAAA

## **FIGURE 26**

MKVLISLLLLLLPLMLMSMVSSSLNPGVARGHRDRGQASRRWLQEGGQECECKDWFLRAPRRKFM  
TVSGLPKKQCPDHFKGNVKKTRHQRHHRKPNKHSRACQQFLKQCQLRSFALPL

**Important features:**

**Signal peptide:**

amino acids 1-22

**N-myristoylation sites.**

amino acids 27-33, 46-52

## FIGURE 27

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGGAAAAAGCCAGTGCCCCAGCGGAAGCACAGCTCAG  
AGCTGGTCTGCCATGGACATCCTGGTCCCCTCCTGCAGCTGCTGGTGTGCTTCTTACCCTGCC  
CCTGCACCTCATGGCTCTGCTGGGCTGCTGGCAGCCCCTGTGCAAAAGCTACTTCCCCTACCTGA  
TGGCCGTGCTGACTCCCAAGAGCAACCGCAAGATGGAGAGCAAGAAACGGGAGCTCTTCAGCCAG  
ATAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGGCCCTACTGGAGCTGGGCTGCCGAACCGGAGC  
CAACTTTTCAGTTCTACCCACCGGGCTGCAGGGTCACCTGCCTAGACCCAAATCCCCACTTTGAGA  
AGTTCCTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATATGAGCGGTTTGTGGTGGCTCCT  
GGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGTGGTGGTCTGCACTCTGGTGTGCTG  
CTCTGTGCAGAGCCCCAAGGAAGGTCTGCAGGAGGTCCGGAGAGTACTGAGACCGGGAGGTGTGC  
TCTTTTTCTGGGAGCATGTGGCAGAACCATATGGAAGCTGGGCCTTCATGTGGCAGCAAGTTTTTC  
GAGCCACCTGGAAACACATTGGGGATGGCTGCTGCCTCACCAGAGAGACCTGGAAGGATCTTGA  
GAACGCCCAGTTCTCCGAAATCCAAATGGAACGACAGCCCCCTCCCTTGAAGTGGCTACCTGTTG  
GGCCCCACATCATGGGAAGGCTGTCAAACAATCTTTCCCAAGCTCCAAGGCACTCATTGTCTCC  
TTCCCCAGCCTCCAATTAGAACAAGCCACCCACCAGCCTATCTATCTTCCACTGAGAGGGACCTA  
GCAGAATGAGAGAAGACATTTCATGTACCACCTACTAGTCCCTCTCTCCCCAACCTCTGCCAGGGC  
AATCTCTAACTTCAATCCCGCCTTCGACAGTGAAAAGCTCTACTTCTACGCTGACCCAGGGAGG  
AAACACTAGGACCCTGTTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCCAACGTTTGCCTC  
CCAATGTTGTCCCTTTCCTTCGTTCCCATGGTAAAGCTCCTCTCGCTTTCCTCCTGAGGCTACAC  
CCATGCGTCTCTAGGAAGTGGTCACAAAAGTCATGGTGCCTGCATCCCTGCCAAGCCCCCTGAC  
CCTCTCTCCCCACTACCACCTTCTTCTGAGCTGGGGGCACCAGGGAGAATCAGAGATGCTGGGG  
ATGCCAGAGCAAGACTCAAAGAGGCAGAGGTTTTGTTCTCAAATATTTTTTAATAAATAGACGAA  
ACCACG

## **FIGURE 28**

MDILVPLLQLLVLLLTPLPLHLMALLGCWQPLCKSYFPYLMVLTTPKSNRKMESKKRELFSSQIKGL  
TGASGKVALLELGCGTGANFQFYPPGCRVTCCLDPNPHFEKFLTKSMAENRHLQYERFVVAPGEDM  
RQLADGSMDEVVCTLVLCVQSPRKVLQEVRRVLRPGGVLEFFWEHVAEPYGSWAFMWQQVFEPTW  
KHIGDGCCLTRETWKDLENAQFSEIQMERQPPPLKWLPGPHIMGKAVKQSFPSKALICSFPSL  
QLEQATHQPIYLPRLGT

### **Important features:**

#### **Signal peptide:**

amino acids 1-23

#### **Leucine zipper pattern.**

amino acids 10-32

#### **N-myristoylation sites.**

amino acids 64-70, 78-84, 80-86, 91-97, 201-207

## **FIGURE 29**

CAATGTTTGCCTATCCACCTCCCCAAGCCCCTTTACCTATGCTGCTGCTAACGCTGCTGCTGCT  
GCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGACTGGTCGGTGCCAGAAAGTCTCTTCTG  
CCACTGACGCCCCCATCAGGGATTGGGCCTTCTTTCCCCCTTCCTTTCTGTGTCTCCTGCCTCAT  
CGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGGAAGGGGAGAAAGTGGGGGATGGCTA  
AGAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGGGTGGGCTAGGGGGGCTGCCTTATTTAAA  
GTGGTTGTTTATGATTCTTATACTAATTTATACAAAGATATTAAGGCCCTGTTTCATTAAGAAATT  
GTTCCCTTCCCCTGTGTTCAATGTTTGTAAAGATTGTTCTGTGTAAATATGTCTTTATAATAAAC  
AGTTAAAAGCTGAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 30**

MLLLTLLLLLLLLLKGSCLWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCSQAQPRG  
EGEKVGDG

**Important features:**

**Signal peptide:**

amino acids 1-15

**Growth factor and cytokines receptors family:**

amino acids 3-18

## FIGURE 31

GTTTGAATTCCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCCAGGCTACCACTT  
CCTCCAAGCAAGTCATTTCCCTTATTTAACCGATGTGTCCCTCAAACACCTGAGTGCTACTCCCT  
ATTTGCATCTGTTTTGATAAATGATGTTGACACCCTCCACCGAATTCTAAGTGGAATCATGTCGG  
GAAGAGATACAATCCTTGGCCTGTGTATCCTCGCATTAGCCTTGTCTTTGGCCATGATGTTTACC  
TTCAGATTCATCACCACCCTTCTGGTTCACATTTTCATTTTCATTGGTTATTTTGGGATTGTTGTT  
TGTCTGCGGTGTTTTATGGTGGCTGTATTATGACTATAACACGACCTCAGCATAGAATTGGACA  
CAGAAAGGGAAAATATGAAGTGCCTGCTGGGGTTTGCTATCGTATCCACAGGCATCACGGCAGTG  
CTGCTCGTCTTGATTTTTGTTCTCAGAAAGAGAATAAAATTGACAGTTGAGCTTTTCCAAATCAC  
AAATAAAGCCATCAGCAGTGCTCCCTTCTGCTGTTCCAGCCACTGTGGACATTTGCCATCCTCA  
TTTTCTTCTGGGTCTCTGGGTGGCTGTGCTGCTGAGCCTGGGAAGTGCAGGAGCTGCCAGGTT  
ATGGAAGGCGGCCAAGTGGAATATAAGCCCTTTTCGGGCATTCCGTACATGTGGTCGTACCATTT  
AATTGGCCTCATCTGGACTAGTGAATTCATCCTTGCGTGCCAGCAAATGACTATAGCTGGGGCAG  
TGGTTACTTGTATTTCACAGAAGTAAAAATGATCCTCCTGATCATCCCATCCTTTCGTCTCTC  
TCCATTCTCTTCTTCTACCATCAAGGAACCGTTGTGAAAGGGTCATTTTTAATCTCTGTGGTGAG  
GATTCCGAGAATCATTGTGATGTACATGCAAAACGCACTGAAAGAACAGCAGCATGGTGCATTGT  
CCAGGTACCTGTTCCGATGCTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTC  
AACCAGAATGCATATACTACAAGTCTATTAATGGGACAGATTTCTGTACATCAGCAAAAGATGC  
ATTCAAAATCTTGTCCAAGAACTCAAGTCACTTTACATCTATTAAGTCTTGGAGACTTCATAA  
TTTTTCTAGGAAAGGTGTTAGTGGTGTGTTTCACTGTTTTTGGAGGACTCATGGCTTTTAACTAC  
AATCGGGCATTCCAGGTGTGGGCAGTCCCTCTGTTATTGGTAGCTTTTTTGCCTACTTAGTAGC  
CCATAGTTTTTTTATCTGTGTTTGAAACTGTGCTGGATGCACTTTTCTGTGTTTTGCTGTGATC  
TGGAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAATTTCTGAGTTTCGTA  
AAAAGGAGCAACAAATTAAACAATGCAAGGGCACAGCAGGACAAGCACTCATTAAAGGAATGAGGA  
GGGAACAGAACTCCAGGCCATTGTGAGATAGATACCCATTAGGTATCTGTACCTGGAAAACATT  
TCCTTCTAAGAGCCATTTACAGAATAGAAGATGAGACCACTAGAGAAAAGTTAGTGAATTTTTTT  
TAAAAAGACCTAATAAACCTATTCTTCCTCAAAA

## **FIGURE 32**

MSGRDTILGLCILALALSLAMFTFRFITLLVHIFISLVILGLLFVCGVLWWLYDYTDNLSIE  
LDTERENMKCVLGFAIVSTGITAVLLVLIFVLRKRIKLTVELFQITNKAISSAPFLFQPLWTF  
ILIFFVVLWVAVLLSLGTAGAAQVMGGQVEYKPLSGIRYMWSYHLIGLIWTSEFILACQQMTIA  
GAVVTCTYFNRSKNPPDPHPILSSLSILFFYHQGTVVKGSFLISVVRIPRIIVMYMQLKEQQHG  
ALSRYLFRCCYCCFWCLDKYLLHLNQAYTTTAINGTDFCTSAKDAFKILSKNSSHFTSINCFGD  
FIIFLGKVLVVCFTVFGGLMAFNYNRAFQVWAVPLLVAFFAYLVAHSFLSVFETVLDALFLCFA  
VDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRNEEGTELQAIVR

### **Important features:**

#### **Signal peptide:**

amino acids 1-20

#### **Putative transmembrane domains:**

amino acids 35-54, 75-97, 126-146, 185-204, 333-350, 352-371

#### **N-glycosylation sites.**

amino acids 204-208, 295-299, 313-317

#### **N-myristoylation sites.**

amino acids 147-153, 178-184, 196-202, 296-275, 342-348



## FIGURE 33

GTTCGATTAGCTCCTCTGAGAAGAAGAGAAAAGGTTCTTGGACCTCTCCCTGTTTCTTCTTAGA  
 ATAATTTGTATGGGATTTGTGATGCAGGAAAGCCTAAGGGAAAAAGAATATTCATTCTGTGTGGT  
 GAAAATTTTTTGAAGAAAAAATTGCCCTTCTTCAAACAAGGGTGTCAATCTGATATTTATGAGGAC  
 TGTGTGTTCTCACTATGAAGGCATCTGTTATTGAAATGTTCTTGTGTTTGTGCTGGTGACTGGAGTAC  
 ATTCAAACAAGAAACGGCAAAGAAGATTAAAGGCCCAAGTTCACTGTGCCTCAGATCAACTGC  
 GATGTCAAAGCCGAAAGATCATCGATCCTGAGTTTATTGTGAAATGTCCAGCAGGATGCCAAGA  
 CCCCAAATACCATGTTTATGGCACTGACGTGTATGCATCCTACTCCAGTGTGTGTGGCGCTGCCG  
 TACACAGTGGTGTGCTTGATAATTAGAGAGGGAAAAATACTTGTTCGGAAGGTTGCTGGACAGTCT  
 GGTTACAAAGGGAGTTATTCCAACGGTGTCCAATCGTTATCCCTACCACGATGGAGAGAATCCTT  
 TATCGTCTTAGAAAGTAAACCCAAAAAGGGTGTAACCTACCCATCAGCTCTTACATACTCATCAT  
 CGAAAAGTCCAGCTGCCCAAGCAGGTGAGACCACAAAAGCCTATCAGAGGCCACCTATTCCAGGG  
 ACAACTGCACAGCCGGTCACTCTGATGCAGCTTCTGGCTGTCACTGTAGCTGTGGCCACCCCCAC  
 CACCTTGCCAAAGGCCATCCCTTCTGCTGCTTCTACCACCAGCATCCCAGACCACAATCAGTGG  
 GCCACAGGAGCCAGGAGATGGATCTCTGTTCCACTGCCACCTACACAAGCAGCCAAAACAGGCC  
 AGAGCTGATCCAGGTATCCAAAGGCAAGATCCTTCAGGAGCTGCCCTTCAGAAACCTGTTGGAGC  
 GGATGTGAGCTGGGACTTGTCCAAAAGAAGAATTGAGCACACAGTCTTGGAGCCAGTATCCC  
 TGGGAGATCCAACTGCAAAATTGACTTGTGCTTTTTTAATTGATGGGAGCACCAGCATTGGCAAA  
 CGGCGATTCCGAATCCAGAAGCAGCTCCTGGCTGATGTTGCCCAAGCTCTTGACATTGGCCCTGC  
 CGGTCCACTGATGGGTGTTGTCCAGTATGGAGACAACCCTGCTACTCACTTTAACCTCAAGACAC  
 ACACGAATTCTCGAGATCTGAAGACAGCCATAGAGAAAATTACTCAGAGAGGAGGACTTTCTAAT  
 GTAGGTCGGGCCATCTCCTTTGTGACCAAGAACTTCTTTTCCAAAGCCAATGGAACAGAAGCGG  
 GGCTCCCAATGTGGTGGTGGTATGGTGGATGGCTGGCCACGGACAAAAGTGGAGGAGGCTTCAA  
 GACTTGCGAGAGAGTCAGGAATCAACATTTCTTCATCACCATTGAAGGTGCTGCTGAAAATGAG  
 AAGCAGTATGTGGTGGAGCCCAACTTTGCAACAAGGCCGTGTGCAGAACAAACGGCTTCTACTC  
 GCTCCACGTGCAGAGCTGGTTTGGCCTCCACAAGACCTGCAGCCTCTGGTGAAGCGGGTCTGCG  
 AACTGACCGCCTGGCCTGCAGCAAGACCTGCTTGAACCTGGCTGACATTGGCTTCGTCATCGAC  
 GGCTCCAGCAGTGTGGGGACGGGCAACTTCCGCACCGTCTCCAGTTTGTGACCAACCTCACCAA  
 AGAGTTTGAGATTTCCGACACGGACACGGCATCGGGGCCGTGCAGTACACCTACGAACAGCGGC  
 TGGAGTTTGGGTTTCGACAAGTACAGCAGCAAGCCTGACATCCTCAACGCCATCAAGAGGGTGGGC  
 TACTGGAGTGGTGGCACCAGCAGGGGGCTGCCATCAACTTCGCCCTGGAGCAGCTCTTCAAGAA  
 GTCCAAGCCCAACAAGAGGAAGTTAATGATCCTCATCACCGACGGGAGGTCTACGACGACGTCC  
 GGATCCAGCCATGGCTGCCCATCTGAAGGGAGTGATCACCTATGCGATAGGCGTTGCCTGGGCT  
 GCCCAAGAGGAGCTAGAAGTCATTGCCACTACCCCGCCAGAGACCTCCTTCTTTGTGGACGA  
 GTTTGACAACCTCCATCAGTATGTCCCCAGGATCATCCAGAACATTTGTACAGAGTTCAACTCAC  
 AGCCTCGGAACGTAATTAGAGCAGGCAGAGCACCAGCAAGTGCTGCTTTACTAAGTACGCTGTT  
 GGACCACCCACCGCTTAATGGGGCACGCACGGTGCATCAAGTCTTGGGCAGGGCATGGAGAAAC  
 AAATGTCTTGTATTATTCTTTGCCATCATGCTTTTTTCATATTCCAAAACCTGGAGTTACAAAGA  
 TGATCACAACGTATAGAATGAGCCAAAAGGCTACATCATGTTGAGGGTGTGGAGATTTTACAT  
 TTTGACAATTGTTTTCAAATAAATGTTCCGAATACAGTGCAGCCCTTACGACAGGCTTACGTAG  
 AGCTTTTGTGAGATTTTTAAGTTGTTATTTCTGATTTGAACTCTGTAACCTCAGCAAGTTTCAT  
 TTTTGTGATGACATGTAGGAATTGCTGAATTAATGTTTAGAAGGATGAAAAATAAAAAAAAAA  
 AA  
 AAAG

## **FIGURE 34**

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEFIVKCPAG  
CQDPKYHVYGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYSNGVQSLSLPRWR  
ESFIVLESKPKKGVITYPSALTYSSSKSPAAQAGETTKAYQRPPIPGTTAQPVTLMQLLAVTVAVA  
TPTTLPRPSPSAASTTSIPRPQSVGHRSEQEMDLWSTATYTSSQNRPRADPGIQRQDPGSAAFQKP  
VGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLSFLIDGSTSIGKRRFRIQKQLLADVAQALDI  
GPAGPLMGVVQYGDNPATFNLKHTNSRDLKTAIEKITQRGGLSNVGRAISFVTKNFFSKANGN  
RSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAENEKQYVVEPNFANKAVCRTNG  
FYSLHVQSWFGLHKTLLQPLVKRVCDDTLACSKTCLNSADIGFVIDGSSSVGTGNFRTLQFVTN  
LTKEFEISDTRIGAVQYTYEQRLQFQDKYSSKPDILNAIKRVGYWSSGTSTGAAINFALQQL  
FKKSKPNKRKLMILITDGRSYDDVRIPAMAAHLKGVITYAIGVAAQEELEVIATHPARHDSFF  
VDEFDNLHQYVPRIIQNICTEFNSQPRN

### **Important features:**

#### **Signal peptide:**

amino acids 1-26

#### **Transmembrane domain:**

amino acids 181-200

#### **N-glycosylation sites.**

amino acids 390-394, 520-524

#### **N-myristoylation sites.**

amino acids 23-29, 93-99, 115-121, 262-268, 367-373, 389-395,  
431-437, 466-472, 509-515, 570-576, 571-577, 575-581, 627-633

#### **Amidation site.**

amino acids 304-308

## FIGURE 35

CCGAGCACAGGAGATTGCCTGCGTTTAGGAGGTGGCTGCGTTGTGGGAAAAGCTATCAAGGAAGAAATTGC  
CAAACCATGTCTTTTTTCTGTTTTTCAGAGTAGTTTACAACAGATCTGAGTGTTTTAATTAAGCATGGAAT  
ACAGAAAACAACAAAAAAGCTTAAGCTTTAATTTTCATCTGGAATTCACAGTTTTCTTAGCTCCCTGGACCC  
GGTTGACCTGTGGCTCTTCCGCTGGCTGCTCTATCAGTGGTGTCTCCGACTACTCACCCGAGTGTA  
AAGAACCTTCGGCTCGCGTGCTTCTGAGCTGCTGTGGATGGCCTCGGCTCTCTGGACTGTCCTTCCGAGTA  
GGATGTCACTGAGATCCCTCAAATGGAGCCTCCTGCTGCTGTCACTCCTGAGTTTCTTTGTGATGTGGTAC  
CTCAGCCTTCCCCACTACAATGTGATAGAACGCTGAAGTGGATGTACTTCTATGAGTATGAGCCGATTTA  
CAGACAAGACTTTCACCTTCACACTTCGAGAGCATTCAAAGTGTCTCATCAAAATCCATTCTGTGTCATT  
TGGTGACCTCCACCCCTCAGATGTGAAAGCCAGGCAGGCCATTAGAGTTACTTGGGGTGAAAAAAGTCT  
TGGTGGGATATGAGGTCTTACATTTTTCTTATTAGGCCAAGAGGCTGAAAGGAAGAACAATGTTGGC  
ATTGTCCTTAGAGGATGAACACCTTCTTTATGGTGACATAATCCGACAAGATTTTTTAGACACATATAATA  
ACCTGACCTTGAAAACCATATGGCATTCAAGTGGGTAAGTGTGTTTGGCCCAATGCCAAGTACGTAATG  
AAGACAGACACTGATGTTTTTCATCAATACTGGCAATTTAGTGAAGTATCTTTTAAACCTAAACCACTCAGA  
GAAGTTTTTCACAGGTTATCCTCTAATTGATAATTATTCTATAGAGGATTTTACCAAAAAACCATATTT  
CTTACCAGGAGTATCCTTTCAAGGTGTTCCCTCCATACTGCAGTGGGTGGGTTATATAATGTCCAGAGAT  
TTGGTGCCAAGGATCTATGAAATGATGGGTACGTAAAACCCATCAAGTTGAAGATGTTTATGTGCGGAT  
CTGTTTGAATTTATTAAGGTGAACATTCATATCCAGAGACACAAATCTTTCTTCTATATAGAATCC  
ATTTGGATGTCTGTCAACTGAGACGTGTGATTGCAGCCCATGGCTTTTCTTCCAAGGAGATCATCACTTTT  
TGGCAGGTGATGCTAAGGAACACCACATGCCATTATTAAGTTTACATTCTACAAAAAGCCTAGAAGGACAG  
GATACCTTGTGGAAAGTGTTAAATAAAGTAGGTACTGTGAAAATTTCATGGGGAGGTCAAGTGTGCTGGCTT  
ACACTGAACTGAACTCATGAAAAACCCAGACTGGAGACTGGAGGGTTACACTTGTGATTATTAGTCAGG  
CCCTTCAAAGATGATATGTGGAGGAATTAATATAAAGGAATTGGAGGTTTTTGCTAAAGAAATTAATAGG  
ACCAACAATTTGGACATGTCATTCTGTAGACTAGAATTTCTTAAAGGGTGTTACTGAGTTATAAGCTCA  
CTAGGCTGTAAAAACAAAACATGTAGAGTTTTATTTATTGAACAATGTAGTCACTTGAAGGTTTTGTGTA  
TATCTTATGTGGATTACCAATTTAAAAATATATGTAGTTCTGTGTCAAAAAACTTCTTCACTGAAGTTATA  
CTGAACAAAATTTACCTGTTTTTGGTCATTTATAAAGTACTTCAAGATGTTGCAGTATTTACAGTTATT  
ATTATTTAAATTAATTCAACTTTGTGTTTTTAAATGTTTTGACGATTTCAATACAAGATAAAAGGATAG  
TGAATCATTTCTTACATGCAACATTTTCCAGTTACTTAACTGATCAGTTTATTATTGATACATCACTCCA  
TTAATGTAAAGTCATAGGTCATTATTGCATATCAGTAATCTCTTGGACTTGTAAATATTTTACTGTGGT  
AATATAGAGAAGAATTAAAGCAAGAAAATCTGAAAA

## **FIGURE 36**

MASALWTVLPSRMSLRSLKWSLLLLLSLLSFFVMWYLSLPHYNVIERVNWMYFYEYEPYRQDFHF  
TLREHSNCSHQNPFLVILVTSHPSDVKARQAIRVTWGEKKSWWGYEVLTFLLGQEAEEKDKMLA  
LSLEDEHLLYGDIIRQDFLDTYNNLTTLKTIMAFRWVTEFCPNAKYVMKTDTDVFINTGNLVKYL  
NLNHSEKFFTGYPLIDNYSYRGFYQKTHISYQEYPFKVFPPYCSGLGYIMSRDLVPRIYEMMGHV  
KPIKFEDVYVGICLNLLKVNHIHIPEDTNLFFLYRIHLDVCQLRRVIAAHGFSSKEIITFWQVMLR  
NTTCHY

### **Important features:**

#### **Type II transmembrane domain:**

amino acids 20-39

#### **N-glycosylation sites.**

amino acids 72-76, 154-158, 198-202, 212-216, 326-330

#### **Glycosaminoglycan attachment site.**

amino acids 239-243

#### **Ly-6 / u-PAR domain proteins.**

amino acids 23-37

#### **N-myristoylation site.**

amino acids 271-277

## FIGURE 37

CGCTCGGGCACCAGCCGCGCAAGGATGGAGCTGGGTTGCTGGACGCAGTTGGGGCTCACTTTTCTTCAGCTCCTTCTCATC  
TCGTCCTTGCCCAAGAGAGTACACAGTCATTAAATGAAGCCTGCCCTGGAGCAGAGTGGAATATCATGTGTCGGGAGTGCTGTG  
AATATGATCAGATTGAGTGCCTCTGCCCGGAAAGAGGGAAGTCGTGGGTTATACCATCCCTTGCTGCAGGAATGAGGAGAA  
TGAGTGTGACTCCTGCCTGATCCACCCAGGTTGTACCATCTTTGAAAAGCTGCAAGAGCTGCCGAAATGGCTCATGGGGGGGT  
ACCTTGGATGACTTCTATGTGAAGGGTTCTACTGTGCAGAGTGCCGAGCAGGCTGGTACGGAGGAGACTGCATGCGATGTG  
GCCAGGTTCTGCGAGCCCCAAGGGTCAGATTTTGTGGAAAGCTATCCCTAAATGCTCACTGTGAATGGACCATTTCATGC  
TAAACCTGGGTTTGTATCCAACTAAGATTTGTATGTTGAGTCTGGAGTTTGACTACATGTGCCAGTATGACTATGTTGAG  
GTTCTGTATGGAGACAACCGCATGGCCAGATCATCAAGCGTGTCTGTGGCAACGAGCGGCCAGCTCCTATCCAGAGCATAG  
GATCTCACTCCACGTCTCTTCCACTCCGATGGCTCCAAGAATTTGACGGTTTCCATGCCATTATGAGGAGATCACAGC  
ATGCTCCTCATCCCTTGTTTCCATGACGGCAGCTGCGTCTTGACAAGGCTGGATCTTACAAGTGTGCTGCTTGGCAGGC  
TATACTGGGCAGCGCTGTGAAAATCTCCTTGAAGAAAGAACTGCTCAGACCCTGGGGGCCAGTCAATGGGTACCAGAAAA  
TAACAGGGGGCCCTGGGCTTATCAACGGACGCCATGCTAAAAATGGCACCCTGGTGTCTTTCTTTTGTAAACACTCCTATGT  
TCTTAGTGGCAATGAGAAAAGAACTTGCCAGCAGAAATGGAGAGTGGTCAGGGAACAGCCCATCTGCATAAAAGCTGCCGA  
GAACCAAAGATTTCAGACCTGGTGAGAAGGAGAGTTCTTCCGATGCAGGTTCAAGGGAGACACCATTAACACAGCTAT  
ACTCAGCGCCCTTCAGCAAGCAGAACTGCAGAGTGCCTTACCAAGAGCCAGCCCTTCCCTTTGGAGATCTGCCCATGGG  
ATACCAACATCTGCATACCCAGCTCCAGTATGAGTGCATCTCACCTTCTACCGCCGCTGGGCAGCAGCAGGAGACATGT  
CTGAGGACTGGGAAGTGGAGTGGCGGGCACCATCTGCATCCCTATCTGCGGGAAAATGAGAACATCACTGCTCCAAAGA  
CCCAAGGGTTGCGCTGGCGTGGCGTGGCAGGACCATCTACAGGAGGACCAGCGGGGTGCATGACGGCAGCCTACACAGGGAGC  
GTGGTTCTAGTCTGCAGCGGTGCCCTGGTGAATGAGCGCACTGTGGTGGTGGCTGCCCATGTGTTACTGACCTGGGGAAG  
GTCACCATGATCAAGACAGCAGACCTGAAAGTTGTTTGGGGAAATCTACCGGGATGATGACCGGGATGAGAAGACCATCC  
AGAGCCTACAGATTCTGCTATCATCTGCATCCCAACTATGACCCCATCTGCTTGATGCTGACATCGCCATCTGAAGCT  
CCTAGACAAGGCCGATATCAGCACCCGAGTCCAGCCCATCTGCCCTGCTGCCAGTCGGGATCTCAGCACTTCTTCCAGGAG  
TCCCACATCACTGTGGCTGGCTGGAATGTCTTGGCAGACGTGAGGAGCCCTGGCTTCAAGAACGACACACTGCGCTCTGGGG  
TGGTCAGTGTGGTGGACTGCTGCTGTGTGAGGAGCAGCATGAGGACCATGGCATCCCACTGAGTGTCACTGATAACATGTT  
CTGTGCCAGCTGGGAACCCACTGCCCTTCTGATATCTGCACTGCAGAGACAGGAGGCATCGCGGCTGTGTCTTCCCGGA  
CGAGCATCTCCTGAGCCAGCTGGCATCTGATGGGACTGGTCAGCTGGAGCTATGATAAAACATGCAGCCACAGGCTCTCCA  
CTGCCCTTACCAAGGTGCTGCCCTTTAAAGACTGGATTGAAAGAAATATGAAATGAACCATGCTCATGCACTCCTTGAGAAG  
TGTTTCTGTATATCCGTCTGTACGTGTGTCATTGCGTGAAGCAGTGTGGCCTGAAGTGTGATTGGCCTGTGAACCTGGCT  
GTGCCAGGGCTTCTGACTTCAGGGACAAAACCTCAGTGAAGGGTGAGTAGACCTCCATTGCTGGTAGGCTGATGCCGCTCCA  
CTACTAGGACAGCCAATTGGAAGATGCCAGGGCTTGCAAGAAGTAAGTTTCTTCAAAGAAGACCATATACAAAACCTCTCCA  
CTCCACTGACCTGGTGGTCTTCCCAACTTTTCAGTTATACGAATGCCATCAGCTTGACCAGGGAAGATCTGGGCTTCATGAG  
GCCCCCTTTGAGGCTCTCAAGTTCTAGAGAGCTGCCCTGTGGGACAGCCAGGGCAGCAGAGCTGGGATGTGGTGCATGCCTT  
TGTGTACATGGCCACAGTACAGTCTGGTCTTTTCTTCCCATCTCTTGTACACATTTTAAATAAAATAGGGTTGGCTTCT  
GAAC TACAAA  
AAA

## **FIGURE 38**

MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECCEYDQIECVCPGKREVVGYT  
IPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGLDDFYVKGFYCAECRAGWYGGDCMRGQ  
VLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRDGDNRDQII  
KRVCGNERPAPIQSIGSSLHVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDGTCVLDKAGSYKC  
ACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTVVSFFCNSYVLSGNE  
KRTCQQNGEWSGKQFICIKACREPKISDLVRRRVLPQVQSRETPHQLYSAAFSKQKLQSAPTK  
KPALPFGDLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPSCIPICGKIENITAP  
KTQGLRWPWQAAIYRRTSGVHDGSLHKGAWFLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADL  
KVVLGKFYRDDDRDEKTIQSLQISAILHPNYDPILLDADIAILKLLDKARISTRVQPICLAASR  
DLSTSFQESHITVAGWNVLADVRSPGFKNDTLRSGVSVVDSLLCEEQHEDHGIPVSVTDNMFCA  
SWEPTAPSDICTAETGGIAAVSFPGRASPEPRWHLMLVSWSYDKTCSHRLSTAFTKVLFPFKDWI  
ERNMK

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-23

#### **EGF-like domain cysteine pattern signature.**

amino acids 260-272

#### **N-glycosylation sites.**

amino acids 96-100, 279-283, 316-320, 451-455, 614-618

#### **N-myristoylation sites.**

amino acids 35-41, 97-103, 256-262, 284-290, 298-304, 308-314,  
474-480, 491-497, 638-644, 666-672

#### **Amidation site.**

amino acids 56-60

#### **Serine proteases, trypsin family.**

amino acids 489-506

#### **CUB domain proteins profile.**

amino acids 150-167

## FIGURE 39

GGTTCCTACATCCTCTCATCTGAGAATCAGAGAGCATAATCTTCTTACGGGCCCCGTGATTATTAAACGTGGCTTAATC  
TGAAGGTTCTCAGTCAAATCTTTGTGATCTACTGATTGTGGGGGCATGGCAAGGTTTGCTTAAAGGAGCTTGGCTGG  
TTTGGGGCCCTTGTAGCTGACAGAAGGTGGCCAGGGAGAATGCAGCACACTGCTCGGAGAATGAAGGCGCTTCTGTTC  
TGGTCTTGCCCTTGGCTCAGTCTGTAACTACATTGACAATGTGGGCAACCTGCACTTCCTGTATTGAGAACTCTGTA  
AAGGTGCCTCCCACTACGGCTGACCAAAGATAGGAAGAGGCGCTCACAAGATGGCTGTCCAGACGGCTGTGCGAGCC  
TCACAGCCACGGCTCCCTCCCAAGGTTTCTGCAGCTGCCACCATCTCCTTAATGACAGACGAGCCTGGCCTAGACA  
ACCTTGCTTACGTGTCTCGGCAGAGGACGGGCAGCCAGCAATCAGCCCAGTGGACTCTGGCCGGAGCAACCGAATA  
GGGCACGGCCCTTTGAGAGATCCACTATTAGAAGCAGATCATTTAAAAAATAAATCGAGCTTTGAGTGTTCTTCGAA  
GGACAAAGAGCGGAGTGCAGTTGCCAACCATGCCGACCAGGGCAGGAAAAATTCTGAAAACACCACTGCCCTGAAG  
TCTTTCCAAGGTTGTACCACTGATTCCAGATGGTGAATTAACAGCATCAAGATCAATCGAGTAGATCCCACTGAAA  
GCCTCTCTATTAGGCTGGTGGGAGGTAGCGAAACCCCACTGGTCCATATCATTATCCAACACATTTATCGTGATGGGG  
TGATCGCCAGAGACGGCCGGCTACTGCCAGGAGACATCATTCTAAAGGTCAACGGGATGGACATCAGCAATGTCCCTC  
ACAACTACGCTGTGCGTCTCCTGCGGCAGCCCTGCCAGGTGCTGTGGCTGACTGTGATGCGTGAACAGAAGTCCGCA  
GCAGGAACAATGGACAGGCCCCGGATGCCACAGCCCCGAGATGACAGCTTTCATGTGATTCTCAACAAAAGTAGCC  
CCGAGGAGCAGCTTGAATAAACTGGTGCAGAGGTGGATGAGCCTGGGGTTTTCATCTTCAATGTGCTGGATGGCG  
GTGTGGCATATCGACATGGTCAGCTTGAGGAGAATGACCGTGTGTAGCCATCAATGGACATGATCTTCGATATGGCA  
GCCCAGAAAGTGGGGTCATCTGATTGAGGCCAGTGAAAGACGTGTTACCTCGTGTGTCGCCAGGTTCCGGCAGC  
GGAGCCCTGACATCTTTCAGGAAGCCGGTGGAACAGCAATGGCAGCTGGTCCCCAGGGCCAGGGGAGAGGAGCAACA  
CTCCCAGCCCTCCATCCTACAATTACTTGTGATGAGAAGGTGGTAAATATCCAAAAAGACCCCGGTGAATCTCTCG  
GCATGACCGTCGCGAGGGGAGCATCACATAGAGAATGGGATTTGCCTATCTATGTCATCAGTGTGAGCCCGGAGGAG  
TCATAAGCAGAGATGGAAGAATAAAACAGGTGACATTTTGTGAATGTGGATGGGTCGAACTGACAGAGGTCAGCC  
GGAGTGAGGCAGTGGCATTATTGAAAGAACATCATCTCGATAGTACTCAAAGCTTTGGAAGTCAAAGAGTATGAGC  
CCCAGGAAGACTGCAGCAGCCAGCAGCCCTGGACTCCAACCACAACATGGCCCCACCCAGTGACTGGTCCCCATCCT  
GGGTGATGTGGCTGGAATTACCACGGTGCTTGATAACTGTAAAGATATTGTATTACGAAGAAACACAGCTGGAAGTC  
TGGGCTTCTGCATTGTAGGAGTTATGAAGAATACAATGGAAACAAACCTTTTTTCATCAAATCCATTGTTGAAGGAA  
CACCAGCATACAATGATGGAAGAATTAGATGTGGTGATATTCTTCTGCTGTCAATGGTAGAAGTACATCAGGAATGA  
TACATGCTTGCTTGGCAAGACTGCTGAAAGAACTTAAAGGAAGAATTACTCTAACTATTGTTTCTTGGCCTGGCACTT  
TTTTATAGGAATCAATGATGGGTGAGAGGAAAAACAGAAAAATCACAAATAGGCTAAGAAGTTGAAACACTATATTTATC  
TTGTGAGTTTTTATATTAAAGAAAGAAATACATTGTAAAAATGTCAGGAAAAGTATGATCATCTAATGAAAGCCAGTT  
ACACCTCAGAAAATATGATTCCAAAAAATAAACTACTAGTTTTTTTTTCAGTGTGGAGGATTTCTCATTACTCTAC  
AACATTGTTTATATTTTTCTATTCAATAAAAGCCCTAAAACAATAAATGATTGATTGTATACCCCACTGAATT  
CAAGCTGATTTAAATTTAAATTTGGTATATGCTGAAGTCTGCCAAGGGTACATTATGGCCATTTTAAATTTACAGCT  
AAAAATATTTTTTAAATGCAATGCTGAGAAACGTTGCTTTTCATCAAACAAGAATAAATATTTTTTCAGAAGTTAAA

## **FIGURE 40**

MKALLLLVLPWLSPANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGCPCDGCASLTATAPS  
PEVSAAATISLMTDEPGLDNPAYVSSAEDGQPAISPVDSGRSNRTRARPFERSTIRSRSFKKINR  
ALSVLRRTKSGSAVANHADQGRENSENTTAPEVFPRLYHLIPDGEITSIKINRVDPSSELSIRLV  
GGSETPLVHIIIQHIYRDGVIARDGRLLPGDIILKVNMGDISNVPHNYAVRLLRQPCQVLWLTVM  
REQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEEQLGIKLVRKVDEPGVFI FNVLDGGVAYRHG  
QLEENDRVLAINGHDLRYGSPESAHLIQASERRVHLVVSQRQVRSPDIFQEAGWNSNGSWSPG  
PGRSNTPKPLHPTITCHEKVVNIQKDPGESLGMTVAGGASHREWDLPIYVISVEPGGVISRDGR  
IKTGDI LLNV DGV ELTEVSRSEAVALLKRTSSSIVLKALEVKEYEPQEDCSSPAALDSNNHMAPP  
SDWSPSWVMWLELPRCLYNCKDIVLRRTAGSLGFCIVGGYEEYNGNKPFFIKSIVEGTPAYNDG  
RIRCGDILLAVNGRSTSGMIHACLARLLKELKGRITLTIVSWPGTFL

### **Important features:**

#### **Signal peptide:**

amino acids 1-15

#### **N-glycosylation sites.**

amino acids 108-112, 157-161, 289-293, 384-388

#### **Tyrosine kinase phosphorylation sites.**

amino acids 433-441, 492-500

#### **N-myristoylation sites.**

amino acids 51-57, 141-147, 233-239, 344-350, 423-429, 447-453,  
467-473, 603-609



## FIGURE 41

ACCAGGCATTGTATCTTCAGTTGTCATCAAGTTCGCAATCAGATTGGAAAAGCTCAACTTGAAGCTTT  
CTTGCCCTGCAGTGAAGCAGAGAGATAGATATTATTACGTAATAAAAAACATGGGCTTCAACCTGACT  
TTCCACCTTTCTACAAATTCGATTACTGTTGCTGTTGACTTTGTGCCTGACAGTGGTTGGGTGGGC  
CACCAGTAACTACTTCGTGGGTGCCATTCAAGAGATTCTTAAAGCAAAGGAGTTCATGGCTAATTTCC  
ATAAGACCTCATTTTGGGGAAGGGAAAACTCTGACTAATGAAGCATCCACGAAGAAGGTAGAACTT  
GACAACGTCTCTTCTGTGTCTCCTTACCTCAGAGGCCAGAGCAAGCTCATTTTCAAACCAGATCTCAC  
TTTGAAGAGGTACAGGCAGAAAATCCCAAAGTGTCCAGAGGCCGGTATCGCCCTCAGGAATGTAAAG  
CTTTACAGAGGGTCGCCATCCTCGTTCCCCACCGAACAGAGAGAAACACCTGATGTACCTGCTGGAA  
CATCTGCATCCCTTCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTCATCCACCAGGCTGAAGG  
TAAAAAGTTTAATCGAGCCAACTCTTGAATGTGGGCTATCTAGAAGCCCTCAAGGAAGAAAATTGGG  
ACTGCTTTATATTCCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAAGTGTGAGGAG  
CATCCCAAGCATCTGGTGGTTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTGGATATTTGG  
GGGTGTTACTGCCCTAAGCAGAGAGCAGTTTTTCAAGGTGAATGGATTCTCTAACAACCTACTGGGGAT  
GGGGAGGCGAAGACGATGACCTCAGACTCAGGGTTGAGCTCCAAAGAATGAAAATTTCCCGGCCCTG  
CCTGAAGTGGGTAAATATACAATGGTCTTCCACACTAGAGACAAAGGCAATGAGGTGAACGCAGAACG  
GATGAAGCTCTTACACCAAGTGTACGAGTCTGGAGAACAGATGGGTTGAGTAGTTGTTCTTATAAAT  
TAGTATCTGTGGAACACAATCCTTTATATATCAACATCACAGTGGATTCTGGTTTGGTGCATGACCC  
TGGATCTTTTGGTGATGTTTGAAGAAGTGAATCTTTGTTTGCAATAATTTTGGCCTAGAGACTTCAA  
ATAGTAGCACACATTAAGAACCTGTTACAGCTCATTGTTGAGCTGAATTTTCTTTTGTATTTTCT  
TAGCAGAGCTCCTGGTGATGTAGAGTATAAAACAGTTGTAACAAGACAGCTTCTTAGTCATTTTGAT  
CATGAGGGTTAAATATTGTAATATGGATACTTGAAGGACTTTATATAAAAGGATGACTCAAAGGATAA  
AATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTATTTAAATTTGAAGTAATATATTATGGGAT  
AAAAGGCCACAGGAAATAAGACTGCTGAATGTCTGAGAGAACCAGAGTTGTTCTCGTCCAAGGTAGAA  
AGGTACGAAGATACAATACTGTTATTTCATTTATCCTGTACAATCATCTGTGAAGTGGTGGTGTGAGGT  
GAGAAGGCGTCCACAAAAGAGGGGAGAAAAGGCGACGAATCAGGACACAGTGAACCTGGGAATGAAGA  
GGTAGCAGGAGGGTGGAGTGTGGCTGCAAAGGCAGCAGTAGCTGAGCTGGTTGCAGGTGCTGATAGC  
CTTCAGGGGAGGACCTGCCAGGTATGCCTTCCAGTGATGCCACCAGAGAATACATTCTCTATTAGT  
TTTTAAAGAGTTTTTGTAAAATGATTTTGTACAAGTAGGATATGAATTAGCAGTTTACAAGTTTACAT  
ATTAACATAATAAATATGTCTATCAAATACCTCTGTAGTAAATGTGAAAAGCAAAA

## **FIGURE 42**

MGFNLTFFHLSYKFRLLLLLTCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTLILGKGKTLTN  
EASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYRPQECKALQRVAILVPH  
RNREKHLMYLLEHLHPFLQRQOLDYGIYVIHQAEKKFNRAKLLNVGYLEALKEENWDCFI FHDV  
DLVPENDFNLYKCEEHPKHLVVGGRNSTGYRLRYSGYFGGVTALSREQFFKVNGFSNNYWGWWGED  
DDLRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAERMKLLHQVSRVWRTDGLSSCSYKLV  
SVEHNPLYINITVDFWFGA

**Important features:**

**Signal peptide:**

amino acids 1-27

**N-glycosylation sites.**

amino acids 4-8, 220-224, 335-339

**Xylose isomerase proteins.**

amino acids 191-202

## **FIGURE 43**

GCTCAAGACCCAGCAGTGGGACAGCCAGACAGACGGCACGATGGCACTGAGCTCCCAGATCTGGG  
CCGCTTGCCTCCTGCTCCTCCTCCTCCTCGCCAGCCTGACCAGTGGCTCTGTTTTCCCACAACAG  
ACGGGACAACCTTGCAGAGCTGCAACCCAGGACAGAGCTGGAGCCAGGGCCAGCTGGATGCCCAT  
GTTCCAGAGGCGAAGGAGGCGAGACACCCACTTCCCCATCTGCATTTTCTGCTGCGGCTGCTGTC  
ATCGATCAAAGTGTGGGATGTGCTGCAAGACGTAGAACCTACCTGCCCTGCCCCCGTCCCCTCCC  
TTCCTTATTTATTCCTGCTGCCCCAGAACATAGGTCTTGGAATAAAATGGCTGGTTCTTTTGTTT  
TCCAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 44**

MALSSQIWAACLLLLLLLLASLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRRDTHFPI  
CIFCCGCCHRSKCGMCCKT

### **Important features:**

#### **Signal peptide:**

amino acids 1-24

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 58-59

#### **N-myristoylation site.**

amino acids 44-50

#### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 1-12

## FIGURE 45

GTGGCTTCATTTTCAGTGGCTGACTTCCAGAGAGCAATATGGCTGGTTCCCCAACATGCCTCACCC  
TCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTGGTCGGT  
TCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTCTATTGTCTG  
GACCTTCAACACAACCCCTCTTGTACCATAACAGCCAGAAGGGGGCACTATCATAGTGACCCAAA  
ATCGTAATAGGGAGAGAGTAGACTTCCAGATGGAGGCTACTCCCTGAAGCTCAGCAAAGTGAAG  
AAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCA  
GGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCA  
ATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATGGAACATGGGGAAGAGGATGTGATT  
TATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTCCCATAATGGGTCCATCCTCCCCATCTC  
CTGGAGATGGGGAGAAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCCGTGCAGCAGAACT  
TCTCAAGCCCCATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCTCCATG  
GTCCTCCTGTGTCTCCTGTTGGTGCCCTCCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTG  
GTTTCTGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTCTGGG  
AAACTCCTAACATATGCCCCATTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAAT  
AGAACAATCCTAAAGGAAGATCCAGCAAATACGGTTTACTCCACTGTGGAAATACCGAAAAAGAT  
GGAAAATCCCCACTCACTGCTCACGATGCCAGACACACCAAGGCTATTTGCCTATGAGAATGTTA  
TCTTAGACAGCAGTGCCTCCCTAAGTCTCTGCTCA

## **FIGURE 46**

MAGSPTCLTLIYILWQLTGSAAAGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVTIQP  
EGGTIIIVTQNRNRERVDFFDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHVYEHLK  
PKVTMGLQSNKNGTCVTNLTCMEHGEEDVIYTWKALGQAANESHNGSILPISWRWGESDMTFIC  
VARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSLFVLGLFLWFLKRERQEEYIE  
EKKRVDICRETPNICPHSGENTYDTIPHTNRTILKEDPANTVYSTVEIPKKMENPHSLLTMPDT  
PRLFAYENVI

### **Important features:**

#### **Signal peptide:**

amino acids 1-22

#### **Transmembrane domain:**

amino acids 224-250

#### **Leucine zipper pattern.**

amino acids 229-251

#### **N-glycosylation sites.**

amino acids 98-102, 142-146, 148-152, 172-176, 176-180, 204-208,  
291-295

## FIGURE 47

GGCTCGAGCGTTTCTGAGCCAGGGGTGACCAATGACCTGCTGCGAAGGATGGACATCCTGCAATGG  
ATTCAAGCCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTGTCAGCT  
TAGTTGAGGAAGACCAATTTTCTCAAACCCCATCTCTTGCTTTGAGTGGTGGTTCCCAGGAATT  
ATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTTGACAGCAAGAAAAAGAGCGTG  
CTGCAACAACAGAACTGGAATGTTTCTTTCATCATTTTTTCAGTGTGATCACAGTCATTGGTGCTC  
TGATTGCATGCTGATATCCATCCAGGCTCTCTTAAAGGTCTCTCATGTGTAATTCTCCAAGC  
AACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGACATTCATCCAGAATCCTTCAA  
CTTGCAAGTGGTTTTTCAATGACTCTTGTCACCTCCTACTGGTTTCAATAAACCCACCAGTAACG  
ACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCCACTTCGATTCTGAAGAAAACAAACATAGG  
CTTATCCACTTCTCAGTATTTTTAGGTCTATTGCTTGTTGGAATTCTGGAGGTCCTGTTTGGGCT  
CAGTCAGATAGTCATCGGTTTCCTTGGCTGTCTGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTG  
TGTAGTTTAATGGGAATAAAATGTAAGTATCAGTAGTTTGAAAAAAAAA

## **FIGURE 48**

MTCCEGWTSCNGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMAIPA  
TTMSLTARKRACCNRTGMFLSSFFSVITVIGALYCLISIQALLKGPLMCNSPSNSNANCEFSL  
KNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDEENKHLIHFVSFVLGL  
LLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV

### **Important features:**

#### **Transmembrane domains:**

amino acids 10-31 (type II), 50-72, 87-110, 191-213

#### **N-glycosylation sites.**

amino acids 80-84, 132-136, 148-152, 163-167

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 223-227

#### **N-myristoylation sites.**

amino acids 22-28, 54-60, 83-89, 97-103, 216-222

#### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 207-218

#### **TNFR/NGFR family cysteine-rich region protein.**

amino acids 4-12



## **FIGURE 49**

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGGTGA  
AGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTGGAGCAG  
ATCCGTGGGCTGCAGACCCCGCCCCAGTGCCTCTCCCCCTGCAGCCCTGCCCTCGAACTGTGA  
**CATGG**GAGAGAGTGACCCTGGCCCTTCTCCTACTGGCAGGCCTGACTGCCTTGGAAGCCAATGACC  
CATTGCGCAATAAAGACGATCCCTTCTACTATGACTGGAAAAACCTGCAGCTGAGCGGACTGATC  
TGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGGCAAATGCAAATACAAGAG  
CAGCCAGAAGCAGCACAGTCTGTACCTGAGAAGGCCATCCCACTCATCACTCCAGGCTCTGCCA  
CTACTTGCT**TGAG**CACAGGACTGGCCTCCAGGGATGGCCTGAAGCCTAACACTGGCCCCCAGCACC  
TCCTCCCCTGGGAGGCCCTTATCCTCAAGGAAGGACTTCTCTCCAAGGGCAGGCTGTTAGGCCCTT  
TTCTGATCAGGAGGCTTCTTTATGAATTAAACTCGCCCCACCACCCCTCA

## **FIGURE 50**

MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGKCKYKS  
SQKQHSPVPEKAIPLITPGSATTC

### **Important features:**

#### **Signal peptide:**

amino acids 1-16

#### **Transmembrane domain:**

amino acids 36-59

#### **N-myristoylation sites.**

amino acids 41-47, 45-51, 84-90

#### **Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7.**

amino acids 54-67

## FIGURE 51

GTGGACTCTGAGAAGCCCAGGCAGTTGAGGACAGGAGAGAGAAGGCTGCAGACCCAGAGGGAGGG  
AGGACAGGGAGTCCGAAGGAGGAGGACAGAGGAGGGCACAGAGACGCAGAGCAAGGGCGGCAAGG  
AGGAGACCCTGGTGGGAGGAAGACACTCTGGAGAGAGAGGGGGCTGGGCAGAGATGAAGTTCCAG  
GGGCCCCCTGGCCTGCCTCCTGCTGGCCCTCTGCCTGGGCAGTGGGAGGCTGGCCCCCTGCAGAG  
CGGAGAGGAAAGCACTGGGACAAATATTGGGGAGGCCCTTGGACATGGCCTGGGAGACGCCCTGA  
GCGAAGGGGTGGGAAAGGCCATTGGCAAAGAGGCCGGAGGGGCAGCTGGCTCTAAAGTCAGTGAG  
GCCCTTGGCCAAGGGACCAGAGAAGCAGTTGGCACTGGAGTCAGGCAGGTTCCAGGCTTTGGCGC  
AGCAGATGCTTTGGGCAACAGGGTCGGGGAAGCAGCCCATGCTCTGGGAAACACTGGGCACGAGA  
TTGGCAGACAGGCAGAAGATGTCATTCGACACGGAGCAGATGCTGTCCGCGGCTCCTGGCAGGGG  
GTGCCTGGCCACAGTGGTGTCTTGGGAACTTCTGGAGGCCATGGCATCTTTGGCTCTCAAGGTGG  
CCTTGGAGGCCAGGGCCAGGGCAATCCTGGAGGTCTGGGGACTCCGTGGGTCCACGGATACCCCG  
GAAACTCAGCAGGCAGCTTTGGAATGAATCCTCAGGGAGCTCCCTGGGGTCAAGGAGGCAATGGA  
GGGCCACCAAACCTTTGGGACCAACACTCAGGGAGCTGTGGCCAGCCTGGCTATGGTTCAGTGAG  
AGCCAGCAACCAGAATGAAGGGTGCACGAATCCCCACCCTCTGGCTCAGGTGGAGGCTCCAGCA  
ACTCTGGGGGAGGCAGCGGCTCACAGTCGGGCAGCAGTGGCAGTGGCAGCAATGGTGACAACAAC  
AATGGCAGCAGCAGTGGTGGCAGCAGCAGTGGCAGCAGCAGTGGCAGCAGCAGTGGCGGCAGCAG  
TGGCGGCAGCAGTGGTGGCAGCAGTGGCAACAGTGGTGGCAGCAGAGGTGACAGCGGCAGTGAGT  
CCTCCTGGGGATCCAGCACCGGCTCCTCCTCCGGCAACCACGGTGGGAGCGGCGGAGGAAATGGA  
CATAAACCCGGGTGTGAAAAGCCAGGGAATGAAGCCCGCGGGAGCGGGGAATCTGGGATTCAGGG  
CTTCAGAGGACAGGGAGTTTCCAGCAACATGAGGGAATAAGCAAAGAGGGCAATCGCCTCCTTG  
GAGGCTCTGGAGACAATTATCGGGGGCAAGGGTCGAGCTGGGGCAGTGGAGGAGGTGACGCTGTT  
GGTGGAGTCAATACTGTGAACCTCTGAGACGTCTCCTGGGATGTTTAACTTTGACACTTTCTGGAA  
GAATTTTAAATCCAAGCTGGGTTTTCATCAACTGGGATGCCATAAACAAGGACCAGAGAAGCTCTC  
GCATCCCGTGACCTCCAGACAAGGAGCCACCAGATTGGATGGGAGCCCCACACTCCCTCCTTAA  
AACACCACCCTCTCATCACTAATCTCAGCCCTTGCCCTTGAAATAAACCTTAGCTGCCCCACAAA  
AA  
AA

code	activity	amount	frequency	location	duration
0	1	1	1	1	1
1	1	1	1	1	1
2	1	1	1	1	1
3	1	1	1	1	1
4	1	1	1	1	1
5	1	1	1	1	1
6	1	1	1	1	1
7	1	1	1	1	1
8	1	1	1	1	1
9	1	1	1	1	1
10	1	1	1	1	1
11	1	1	1	1	1
12	1	1	1	1	1
13	1	1	1	1	1
14	1	1	1	1	1
15	1	1	1	1	1
16	1	1	1	1	1
17	1	1	1	1	1
18	1	1	1	1	1
19	1	1	1	1	1
20	1	1	1	1	1
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25	1	1	1	1	1
26	1	1	1	1	1
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29	1	1	1	1	1
30	1	1	1	1	1
31	1	1	1	1	1
32	1	1	1	1	1
33	1	1	1	1	1
34	1	1	1	1	1
35	1	1	1	1	1
36	1	1	1	1	1
37	1	1	1	1	1
38	1	1	1	1	1
39	1	1	1	1	1
40	1	1	1	1	1
41	1	1	1	1	1
42	1	1	1	1	1
43	1	1	1	1	1
44	1	1	1	1	1
45	1	1	1	1	1
46	1	1	1	1	1
47	1	1	1	1	1
48	1	1	1	1	1
49	1	1	1	1	1
50	1	1	1	1	1
51	1	1	1	1	1
52	1	1	1	1	1
53	1	1	1	1	1
54	1	1	1	1	1
55	1	1	1	1	1
56	1	1	1	1	1
57	1	1	1	1	1
58	1	1	1	1	1
59	1	1	1	1	1
60	1	1	1	1	1
61	1	1	1	1	1
62	1	1	1	1	1
63	1	1	1	1	1
64	1	1	1	1	1
65	1	1	1	1	1
66	1	1	1	1	1
67	1	1	1	1	1
68	1	1	1	1	1
69	1	1	1	1	1
70	1	1	1	1	1
71	1	1	1	1	1
72	1	1	1	1	1
73	1	1	1	1	1
74	1	1	1	1	1
75	1	1	1	1	1
76	1	1	1	1	1
77	1	1	1	1	1
78	1	1	1	1	1
79	1	1	1	1	1
80	1	1	1	1	1
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82	1	1	1	1	1
83	1	1	1	1	1
84	1	1	1	1	1
85	1	1	1	1	1
86	1	1	1	1	1
87	1	1	1	1	1
88	1	1	1	1	1
89	1	1	1	1	1
90	1	1	1	1	1
91	1	1	1	1	1
92	1	1	1	1	1
93	1	1	1	1	1
94	1				

Signal peptide:

N-glycosylation site.

Glycosaminoglycan attachment site.

Casein kinase II phosphorylation site.

N-myristoylation site.

Cell attachment sequence.

APP ID=10063597

## FIGURE 53

GGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCGACAGAAGGATGTCGCTGCTGAGCCTGCCCTGG  
CTGGGCCTCAGACCGGTGGCAATGTCCCATGGCTACTCCTGCTGCTGGTTGTGGGCTCCTGGCT  
ACTCGCCCGCATCCTGGCTTGGACCTATGCCTTCTATAACAAC TGCCCGGCTCCAGTGTTTCC  
CACAGCCCCAAAACGGAAC TGTTTTGGGGTCACCTGGGCCTGATCACTCCTACAGAGGAGGGC  
TTGAAGGACTCGACCCAGATGTGCGCCACCTATTCCAGGGCTTTACGGTATGGCTGGGTCCCAT  
CATCCCCCTTCATCGTTTTATGCCACCCTGACACCATCCGGTCTATCACC AATGCCTCAGCTGCCA  
TTGCACCCAAGGATAATCTCTTCATCAGGTTCTGAAGCCCTGGCTGGGAGAAGGGATACTGCTG  
AGTGGCGGTGACAAGTGGAGCCGCCACCGTCGGATGCTGACGCCCGCCTTCCATTTCAACATCCT  
GAAGTCCTATATAACGATCTTCAACAAGAGTGCAAACATCATGCTTGACAAGTGGCAGCACCTGG  
CCTCAGAGGGCAGCAGTCGTCTGGACATGTTTGAGCACATCAGCCTCATGACCTTGGACAGTCTA  
CAGAAATGCATCTTCAGCTTTGACAGCCATTGTCAGGAGAGGCCCAGTGAATATATTGCCACCAT  
CTTGAGCTCAGTGCCCTTGTAGAGAAAAGAAGCCAGCATATCCTCCAGCACATGGACTTTCTGT  
ATTACCTCTCCCATGACGGGCGGCGCTTCCACAGGGCCTGCCGCTGGTGCATGACTTCACAGAC  
GCTGTCATCCGGGAGCGCGTCGCACCCTCCCCACTCAGGGTATTGATGATTTTTTCAAAGACAA  
AGCCAAGTCCAAGACTTTGGATTTTCATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGG  
CATTGTGATGAGGATATAAGAGCAGAGGCTGACACCTTCATGTTTGGAGGCCATGACACCAG  
GCCAGTGGCCTCTCCTGGGTCTGTACAACCTTGCGAGGCACCCAGAATACCAGGAGCGCTGCCG  
ACAGGAGGTGCAAGAGCTTCTGAAGACCGCGATCCTAAAGAGATTGAATGGGACGACCTGGCCC  
AGCTGCCCTTCTGACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCAGCTCCCTTCATC  
TCCCGATGCTGCACCCAGGACATTGTTCTCCAGATGGCCGAGTCATCCCCAAGGCATTACCTG  
CCTCATCGATATTATAGGGGTCCATCACACCCAAC TGTGTGGCCGGATCCTGAGGTCTACGACC  
CCTTCCGCTTTGACCCAGAGAACAGCAAGGGGAGGTCACCTCTGGCTTTTATTCCTTTCTCCGCA  
GGGCCCAGGAAC TGCATCGGGCAGGCGTTGCCATGGCGGAGATGAAAGTGGTCCCTGGCGTTGAT  
GCTGCTGCACTTCCGTTTCTGCCAGACCACACTGAGCCCCGAGGAAGCTGGAATTGATCATGC  
GCGCCGAGGGCGGGCTTTGGCTGCGGGTGGAGCCCTGAATGTAGGCTTGCA GTGACTTTCTGAC  
CCATCCACCTGTTTTTTTGCAATTGTCATGAATAAAACGGTGCTGTCAA

## **FIGURE 54**

MSLLSLPWLGLRPVAMSPWLLLLLVVGSWLLARILAWTYAFYNNCRRLQCFPQPPKRNWFWGHLG  
LITPTEEGLKDSTQMSATYSQGFTVWLGPIIPFIVLCHPDTIRSITNASAAIAPKDNLFIRFLKP  
WLGE GILLSGGDKWSRHRRLTPAFHFNLKSYITIFNKSANIMLDKWQHLASEGSSRLDMFEHI  
SLMTLDSLQKCIFSFDSHCQERPSEYIATILELSALVEKRSQHILQHMDFLYYLSHDGRRFHRAC  
RLVHDFTDVIRERRRTLPTQGIDDFKDKAKSKTLD FIDVLLLSKDEDGKALSDEDIRAEADTF  
MFGGHDTTASGLSWVLYNLARHPEYQERCQEVQELLKDRDPKEIEWDDLAQLPFLTMCVKESLR  
LHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVWPDPEVYDPFRFDPENSKGRSP  
LAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHTEPRRKLELIMRAEGGLWLRVEPLN  
VGLQ

### **Important features:**

#### **Transmembrane domains:**

amino acids 13-32 (type II), 77-102

#### **Cytochrome P450 cysteine heme-iron ligand signature.**

amino acids 461-471

#### **N-glycosylation sites.**

amino acids 112-116, 168-172

## FIGURE 55

ATCGCATCAATTGGGAGTACCATCTTCCTCATGGGACCAGTGAAACAGCTGAAGCGAATGTTTGA  
GCCTACTCGTTTGATTGCAACTATCATGGTGCTGTTGTGTTTTGCACTTACCCTGTGTTCTGCCT  
TTGGTGGCATAACAAGGGACTTGCACTTATCTTCTGCATTTTGCAGTCTTTGGCATTGACGTGG  
TACAGCCTTTCCTTCATACCATTTGCAAGGGATGCTGTGAAGAAGTGTTTTGCCGTGTGCTTGC  
ATAATTTCATGGCCAGTTTTATGAAGCTTTGGAAGGCACTATGGACAGAAGCTGGTGGACAGTTTT  
GTAACATCTTCGAAACCTCTGTCTTACAGACATGTGCCTTTTATCTTGCAGCAATGTGTTGCTT  
GTGATTGGAACATTTGAGGGTTACTTTTGAAGCAACAATACATTCTCGAACCTGAATGTCAGTA  
GCACAGGATGAGAAGTGGGTTCTGTATCTTGTGGAGTGGAATCTTCCTCATGTACCTGTTTCCTC  
TCTGGATGTTGTCCCACTGAATTCCCATGAATACAAACCTATTTCAGCAACAGCAAAAAAAAAAAAA  
AA

## **FIGURE 56**

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCILQSLALTWYSLSFIPFAR  
DAVKKCFVCLA

**Important features:**

**Signal peptide:**

amino acids 1-33

**Type II fibronectin collagen-binding domain protein.**

amino acids 30-72



# FIGURE 57

CGGCTCGAGCTCGAGCCGAATCGGCTCGAGGGGCGAGTGGAGCACCCAGCAGGCGGCCAACATGCTCTGTCTGTGCCTG  
TACGTGCCGGTTCATCGGGGAAGCCAGACCGAGTTCCAGTACTTTGAGTCCAAGGGGCTCCCTGCCGAGCTGAAGTCC  
ATTTTCAAGCTCAGTGTCTTCATCCCCCTCCAGGAATTCTCCACCTACCGCCAGTGGAGCAGAAAATTGTACAAGCT  
GGAGATAAGGACCTTGATGGGCAGCTAGACTTTGAAGAATTTGTCCATTATCTCCAAGATCATGAGAAGAAGCTGAGG  
CTGGTGTTTAAGATTTTGGACAAAAGAATGATGGACGCATTGACGCGCAGGAGATCATGCAGTCCCTGCGGGACTTG  
GGAGTCAAGATATCTGAACAGCAGGCAGAAAAAATCTCAAGAGCATGGATAAAAACGGCACGATGACCATCGACTGG  
AACGAGTGGAGAGACTACCACTCCTCCACCCCGTGGAAAACATCCCCGAGATCATCTCTACTGGAAGCATTCACG  
ATCTTTGATGTGGGTGAGAATCTAACGGTCCCGGATGAGTTACAGTGGAGGAGAGGCGACGCGGGATGTGGTGGAGA  
CACCTGGTGGCAGGAGGTGGGGCAGGGGCCGTATCCAGAACCTGCACGGCCCCCTGGACAGGCTCAAGGTGCTCATG  
CAGGTCCATGCCCTCCCGCAGCAACAACATGGGCATCGTTGGTGGCTTCACTCAGATGATTCGAGAAGGAGGGGCCAGG  
TCACCTCTGGCGGGGCAATGGCATCAACGTCCTCAAAATTGCCCGCAATCAGCCATCAAATTCATGGCCTATGAGCAG  
ATCAAGCGCCTTGTGGTAGTGACCAAGAGACTCTGAGGATTCAGGAGGCTTGTGGCAGGGTCCCTGGCAGGGGCC  
ATCGCCAGAGCAGCATCTACCCAATGGAGGTCCCTGAAGACCGGATGGCGCTGCGGAAGACAGGGCCAGTACTCAGGA  
ATGCTGGACTGCCCCAGGAGGATCCTGGCCAGAGAGGGGTGGCCGCTTCTACAAAGGCTATGTCCCCAACATGCTG  
GGCATCATCCCTATGCCGCGCATCGACCTTGAGTCTACGAGACGCTCAAGAATGCCCTGGCTGCAGCAGTATGCAGTG  
AACAGCGCGGACCCCGGCGTGTGGTCTCTGGCCTGTGGCACCATTGTCCAGTACCTGTGGCCAGCTGGCCAGCTAC  
CCCCGGCCCTAGTACGAGACCCGATGACAGGCGCAAGCCTCTATTGAGGGCGCTCCGGAGGTGACCATGAGCAGCCTC  
TTCAACATATCTGCGGACCGAGGGGGCCTTCGGGCTGTACAGGGGGCTGGCCCCCACTTCATGAAGGTGATCCCA  
GCTGTGAGCATCAGCTACGTGGTCTACGAGAACCTGAAGATCACCTGGGCGTGCAGTCCGGTGGAGGGGAGGGC  
CGCCCGGCGAGTGGACTCGCTGATCCTGGGCGCAGCCTGGGGTGTGCAGCCATCTCATCTGTGAATGTGCCAACAT  
AAGCTGTCTCGAGCCAAGCTGTGAAAACCTAGACGCACCCGAGGAGGGTGGGGAGAGCTGGCAGGCCAGGGCTT  
GTCTGTGCTGACCCAGCAGACCTCCTGTTGGTTCAGCGAAGACCACAGGCATTCTTAGGGTCCAGGGTGCAGCAG  
CTCCGGGCTCACATGTGTAAGGACAGGACATTTCTGCAGTGCTGCCAATAGTGAGCTTGGAGCCTGGAGGCCGGCT  
TAGTCTCTCCATTTACCCCTTGCAGCCAGCTGTTGGCCACGGCCCCCTGCCCTCTGGTCTGCCGTGCATCTCCCTGTGC  
CCTCTGTCTGCCCTGCTGTCTGCTGAGTAAGGTGGGAGGAGGGCTACAGCCACATCCACCCCCCTCGTCCAATCCC  
ATAATCCATGATGAAAGGTGAGGTACGTGGCCTCCAGGCCCTGACTTCCCAACCTACAGCATGACGCCAATTGGC  
TGTGAAGGAAGAGGAAGGATCTGGCCTTGTGGTCACTGGCATCTGAGCCCTGCTGATGGCTGGGGCTCTCGGGCATG  
CTTGGGAGTGCAGGGGGCTCGGGTGCCTGGCCTGGCTGCACAGAAGGCAAGTGTGGGGCTCATGGTGTCTGAGCT  
GGCCTGGACCCCTGTGAGGATGGGGCCACCTCAGAACCAACTCACTGTCCCCACTGTGGCATGAGGGCAGTGGAGCA  
CCATGTTTGAGGGCGAAGGGCAGAGCGTTTGTGTCTGGGGAGGGAAGGAAAAGGTGTTGGAGGCCTTAATTATGG  
ACTGTTGGGAAAAGGGTTTTGTCCAGAAGGACAAGCCGACAAATGAGCGACTTCTGTGCTTCCAGAGGAAGACGAGG  
GAGCAGGAGCTTGGCTGACTGCTCAGAGTCTGTTCTGACGCCCTGGGGGTTCTGTCCAACCCAGCAGGGGGCGCAGC  
GGGACCGAGCCCCACATTCCTTGTGTCACTGCTTGGAACTATTTATTTTGTATTTATTTGAACAGAGTTATGTCTCT  
AACTATTTTATAGATTTGTTTAATTAATAGCTTGTCTTTTCAAGTTCATTTTATTTATCATATTTATGTTTATGGTT  
GATTGTACCTTCCCAAGCCCCCAGTGGGATGGGAGGAGGAGGAGAGGGGGGCTTGGGGCGCTGCAGTCACATCT  
GTCCAGAGAAATTCCTTTTGGGACTGGAGGCAGAAAAGCGGCCAGAAAGGCAGCAGCCCTGGCTCCTTTCTTTGGCAG  
GTTGGGGAAAGGGCTTGCCCCAGCCTTAGGATTTAGGGTTTGAAGTGGGGGCGTGGAGAGAGAGGGAGGAACTCAAT  
AACCTTGAAGGTGGAATCCAGTTATTTCTGCGCTGCGAGGGTTCTTTATTTCACTCTTTTCTGAATGTCAAGGCAG  
TGAGGTGCTCTCACTGTGAATTTGTGGTGGGGGGGGCTGGAGGAGAGGGTGGGGGGCTGGCTCCCTCCCTCCAGC  
CTTCTGCTGCCCTTGTCTTAACAATGCCGGCCAACTGGCGACCTCACGGTTGCATTTCCATTCCACCAGAAATGACCTGA  
TGAGGAAATCTTCAATAGGATGCAAGATCAATGCAAAAATTTGTATATATGAACATATAACTGGAGTCTGCAAAAAG  
CAAAATTAAGAAAGAAATGGACGTTAGAAGTTGTCAATTAAGCAGCCTTCTAATAAAGTTGTTTCAAAGCTGAAAAAA  
AA

## **FIGURE 58**

MLCLCLYVPVIGEAQTEFQYFESKGLPAELKSIFKLSVFIPSQEFSTYRQWKQKIVQAGDKDLG  
QLDFEEFVHYLQDHEKKLRLVFKILDKNDGRIDAQEIFMQSLRDLGVKISEQQAEKILKSMDKNG  
TMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLTPDEFTVEERQTMWWRHLVAGGG  
AGAVSRTCTAPLDRLKVLQVHASRSNNMGIVGGFTQMIREGGARSLWRGNGINVLKIAPESAIAK  
FMAYEQIKRLVGSQDETLEIRHERLVAGSLAGAIQSSIYPMEVLKTRMALRKTGGYSGMLDCARR  
ILAREGVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNWLQHYAVNSADPGVFVLLACGTMSSTC  
GQLASYPLALVRTRMQAQASIEGAPEVTMSSLFKHILRTEGAFGLYRGLAPNFMKVIPAVSISYV  
VYENLKITLGVSQR

### **Important features:**

#### **Signal peptide:**

amino acids 1-16

#### **Putative transmembrane domains:**

amino acids 284-304, 339-360, 376-394

#### **Mitochondrial energy transfer proteins signature.**

amino acids 206-215, 300-309

#### **N-glycosylation sites.**

amino acids 129-133, 169-173

#### **Elongation Factor-hand calcium-binding protein.**

amino acids 54-73, 85-104, 121-140

## FIGURE 59

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCCAGCCATGGC  
TTCCCTGGGGCAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAGCAATTG  
CACTCATCATTGGCTTTGGTATTTTCAGGGAGACACTCCATCACAGTCACTACTGTCGCCTCAGCT  
GGGAACATTGGGGAGGATGGAATCCTGAGCTGCACCTTTGAACCTGACATCAAACCTTTCTGATAT  
CGTGATACAATGGCTGAAGGAAGGTGTTTTAGGCTTGGTCCATGAGTTCAAAGAAGGCAAAGATG  
AGCTGTGCGAGCAGGATGAAATGTTTCAGAGGCCGGACAGCAGTGTGCTGATCAAGTGATAGTT  
GGCAATGCCTCTTTGCGGCTGAAAAACGTGCAACTCACAGATGCTGGCACCTACAAATGTTATAT  
CATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATAAACTGGAGCCTTCAGCATGCCGG  
AAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTGGGTTGTGAGGCTCCCCGATGGTTCCCC  
CAGCCCACAGTGGTCTGGGCATCCCAAGTTGACCAGGGAGCCAACCTCTCGGAAGTCTCCAATAC  
CAGCTTTGAGCTGAACTCTGAGAATGTGACCATGAAGGTTGTGTCTGTGCTCTACAATGTTACGA  
TCAACAACACATACTCCTGTATGATTGAAAATGACATTGCCAAAGCAACAGGGGATATCAAAGTG  
ACAGAATCGGAGATCAAAGGCGGAGTCACCTACAGCTGCTAAACTCAAAGGCTTCTCTGTGTGT  
CTCTTCTTTCTTTGCCATCAGCTGGGCACCTTCTGCCTCTCAGCCCTTACCTGATGCTAAAATAAT  
GTGCCTTGGCCACAAAAAGCATGCAAAGTCATTGTTACAACAGGGATCTACAGAACTATTTTAC  
CACCAGATATGACCTAGTTTTATATTTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTG  
AGCAAACAAGAGCAAGAAACAAAAAGAAGCCAAAGCAGAAGGCTCCAATATGAACAAGATAAAT  
CTATCTTCAAAGACATATTAGAAGTTGGGAAAATAATTGATGTGAACTAGACAAGTGTGTTAAGA  
GTGATAAGTAAATGCACGTGGAGACAAGTGCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGT  
CACCTGGGGAGTGAGAGGACAGGATAGTGCATGTTCTTTGTCTCTGAATTTTTAGTTATATGTGC  
TGTAATGTTGCTCTGAGGAAGCCCCTGGAAAGTCTATCCCAACATATCCACATCTTATATCCAC  
AAATTAAGCTGTAGTATGTACCCTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAGGGGCG  
GCTGCATTTTAGTAATGGGTCAAATGATTCACCTTTTTATGATGCTTCCAAAGGTGCCTTGGCTTC  
TCTTCCCAACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAAACAGAGCAGT  
CGGGGACACCGATTTTATAAATAAACTGAGCACCTTCTTTTAAACAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 60**

MASLGQILFWSIISIIIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDIKLS  
DIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASLRLKNVQLTDAGTYKC  
YIITSKGKGNANLEYKTGAFSMPEVNVVDYNASSETLRCEAPRWFPQPTVVWASQVDQGANFSEVS  
NTSFELNSENVTMKVVSVLNVNTINNTYSCMIENDIAKATGDIKVTSEIKRRSHLQLLSKASL  
CVSSFFAISWALLPLSPYMLK

### **Important features:**

#### **Signal peptide:**

amino acids 1-28

#### **Transmembrane domain:**

amino acids 258-281

#### **N-glycosylation sites.**

amino acids 112-116, 160-164, 190-194, 196-200, 205-209, 216-220,  
220-224

#### **N-myristoylation sites.**

amino acids 52-58, 126-132, 188-194

## FIGURE 61

TGACGTCAGAATCACCATGGCCAGCTATCCTTACCGGCAGGGCTGCCAGGAGCTGCAGGACAAG  
CACCAGGAGCCCCCTCCGGGTAGCTACTACCCTGGACCCCCCAATAGTGGAGGGCAGTATGGTAGT  
GGGCTACCCCCTGGTGGTGGTTATGGGGGTCTGCCCTGGAGGGCCTTATGGACCACCAGCTGG  
TGGAGGGCCCTATGGACACCCCAATCCTGGGATGTTCCCTCTGGAACTCCAGGAGGACCATATG  
GCGGTGCAGCTCCCGGGGGCCCCCTATGGTCAGCCACCTCCAAGTTCCTACGGTGCCAGCAGCCT  
GGGCTTTATGGACAGGGTGGCGCCCCCTCCAATGTGGATCCTGAGGCCTACTCCTGGTTCCAGTC  
GGTGGACTCAGATCACAGTGGCTATATCTCCATGAAGGAGCTAAAGCAGGCCCTGGTCAACTGCA  
ATTGGTCTTCAATCAATGATGAGACCTGCCTCATGATGATAAACATGTTTGACAAGACCAAGTCA  
GGCCGCATCGATGTCTACGGCTTCTCAGCCCTGTGGAAATTCATCCAGCAGTGAAGAACCTCTT  
CCAGCAGTATGACCGGGACCGCTCGGGCTCCATTAGCTACACAGAGCTGCAGCAAGCTCTGTCCC  
AAATGGGCTACAACCTGAGCCCCAGTTACCCAGCTTCTGGTCTCCCGCTACTGCCCACGCTCT  
GCCAATCCTGCCATGCAGCTTGACCGCTTCATCCAGGTGTGCACCCAGCTGCAGGTGCTGACAGA  
GGCCTTCCGGGAGAAGGACACAGCTGTACAAGGCAACATCCGGCTCAGCTTCGAGGACTTCGTCA  
CCATGACAGCTTCTCGGATGCTATTGACCCAACCATCTGTGGAGAGTGGAGTGACCAGGGACCTT  
TCCTGGCTTCTTAGAGTGAGAGAAGTATGTGGACATCTCTTCTTTTCCTGTCCCTCTAGAAGAAC  
ATTCTCCCTTGCTTGATGCAACACTGTTCCAAAAGAGGGTGGAGAGTCTGCATCATAGCCACCA  
AATAGTGAGGACCGGGGCTGAGGCCACACAGATAGGGGCTGATGGAGGAGAGGATAGAAGTTGA  
ATGTCCTGATGGCCATGAGCAGTTGAGTGGCACAGCCTGGCACCAGGAGCAGGTCCTTGTAATGG  
AGTTAGTGTCCAGTCAGCTGAGCTCCACCCTGATGCCAGTGGTGAAGTTCATCGGCCTGTTACC  
GTTAGTACCTGTGTTCCCTCACCAGGCCATCCTGTCAAACGAGCCCATTTTCTCCAAAGTGGAAAT  
CTGACCAAGCATGAGAGAGATCTGTCTATGGGACCAGTGGCTTGATTCTGCCACACCCATAAAT  
CCTTGTGTGTTAACTTCTAGCTGCCTGGGGCTGGCCCTGCTCAGACAAATCTGCTCCCTGGGCAT  
CTTTGGCCAGGCTTCTGCCCCCTGCAGCTGGGACCCCTCACTTGCTGCCATGCTCTGCTCGGCT  
TCAGTCTCCAGGAGACAGTGGTCACCTCTCCCTGCCAATACTTTTTTTAATTTGCATTTTTTTTC  
ATTTGGGGCCAAAAGTCCAGTGAAATTGTAAGCTTCAATAAAAGGATGAAACTCTGA

## **FIGURE 62**

MASYPYRQGCPGAAGQAPGAPPGSYYPGPPNSGGQYGSGLPPGGGYGGPAPGGPYGPPAGGGPYG  
HPNPGMFPSGTPGGPYGGAAPGGPYGQPPSSYGAQQPGLYGQGGAPPNVDPEAYSWFQSVDSH  
SGYISMKELKQALVNCNWSSFNDETCLMMINMFDKTKSGRIDVYGFSALWKFIQQWKNLFQQYDR  
DRSGSISYTELQQALSQMGYNLSPQFTQLLVSRYCPRSANPAMQLDRFIQVCTQLQVLTEAFREK  
DTAVQGNIRLSFEDFVTMTASRML

**Important features of the protein:**

**Signal peptide:**

amino acids 1-19

**N-glycosylation site.**

amino acids 147-150

**Casein kinase II phosphorylation sites.**

amino acids 135-138, 150-153, 202-205, 271-274

**N-myristoylation sites.**

amino acids 9-14, 15-20, 19-24, 33-38, 34-39, 39-44, 43-48, 61-66, 70-75, 78-83, 83-88, 87-92, 110-115

## FIGURE 63

CAGGATGCAGGGCCGCGTGGCAGGGAGCTGCGCTCCTCTGGGCCTGCTCCTGGTCTGTCTTCATC  
TCCCAGGCCTCTTTGCCCCGAGCATCGGTGTTGTGGAGGAGAAAGTTTCCCAAACTTCGGGACC  
AACTTGCCCTCAGCTCGGACAACCTTCCTCCACTGGCCCCCTCTAACTCTGAACATCCGCAGCCCGC  
TCTGGACCCTAGGTCTAATGACTTGGCAAGGGTTCCTCTGAAGCTCAGCGTGCCTCCATCAGATG  
GCTTCCCACCTGCAGGAGGTTCTGCAGTGCAGAGGTGGCCTCCATCGTGGGGGCTGCCTGCCATG  
GATTCTGGCCCCCTGAGGATCCTTGGCAGATGATGGCTGCTGCGGCTGAGGACCGCTGGGGGA  
AGCGCTGCCTGAAGAACTCTCTTACCTCTCCAGTGCTGCGGCCCTCGCTCCGGGCAGTGGCCCTT  
TGCCTGGGGAGTCTTCTCCCGATGCCACAGGCCTCTCACCTGAGGCTTCACTCCTCCACCAGGAC  
TCGGAGTCCAGACGACTGCCCCGTTCTAATTCAGTGGGAGCCGGGGGAAAAATCCTTTCCCAACG  
CCCTCCCTGGTCTCTCATCCACAGGGTTCCTGCCTGATCACCCCTGGGGTACCCTGAATCCCAGTG  
TGTCCTGGGGAGGTGGAGGCCCTGGGACTGGTTGGGGAACGAGGCCCATGCCACACCCTGAGGGA  
ATCTGGGGTATCAATAATCAACCCCCAGGTACCAGCTGGGGAAATATTAATCGGTATCCAGGAGG  
CAGCTGGGGAAATATTAATCGGTATCCAGGAGGCAGCTGGGGGAATATTAATCGGTATCCAGGAG  
GCAGCTGGGGGAATATTCATCTATACCCAGGTATCAATAACCCATTTCCTCCTGGAGTTCTCCGC  
CCTCCTGGCTCTTCTTGGAACATCCCAGCTGGCTTCCCTAATCCTCCAAGCCCTAGGTTGCAGTG  
GGGCTAGAGCAGATAGAGGGAAACCCAACATTGGGAGTTAGAGTCCTGCTCCCGCCCCCTTGCTG  
TGTGGGCTCAATCCAGGCCCTGTAAACATGTTTCCAGCACTATCCCCACTTTTCAGTGCCTCCCC  
TGCTCATCTCCAATAAAATAAAAGCAC TTATGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAA

## **FIGURE 64**

MQGRVAGSCAPLG LLLVCLHLPGLFARSIGVVEEKVSNFGTNLPQLGQPSSTGSPNSEHPQPAL  
DPRSNDLARVPLKLSVPPSDGFPFAGGS AVQRWPPSWGLPAMDSWPPEDPWQMAAAAEDRLGEA  
LPEELSYLSSAAALAPGSGPLPGESSPDATGLSPEASLLHQDSESRRLPRSNSLGAGGKILSQRP  
PWSLIHRVLPDHPWGTLNPSVSWGGGGPGTGWGTRMPHPEGIWGINNQPPGT SWGNINRYPGGS  
WGNINRYPGGSWGNINRYPGGSWGNIHLYPGINNPFPPGVLRPPGSSWNIPAGFPNPPSPRLQWG

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

**Casein kinase II phosphorylation sites.**

amino acids 56-59, 155-158

**N-myristoylation sites.**

amino acids 48-53, 220-225, 221-226, 224-229, 247-252, 258-263,  
259-264, 269-274, 270-275, 280-285, 281-286, 305-310



## **FIGURE 65**

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACTATGGGGTC  
TGGGCTGCCCCCTTGTCCTCCTCTTGACCTCCTTGGCAGCTCACATGGAACAGGCCGGGTATGA  
CTTTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCCTGGAA  
TTGCTTGAAAAGCTCTGCCTCCTCCTCCATCTCCCTTCAGGGACCAGCGTCACCTCCACCATGC  
AAGATCTCAACACCATGTTGTCTGCAACACATGACAGCCATTGAAGCCTGTGTCTTCTTGGCCC  
GGGCTTTTGGGCCGGGGATGCAGGAGGCAGGCCCGACCTGTCTTTCAGCAGGCCCCACCTC  
CTGAGTGGCAATAAATAAAATTCGGTATGCTG

## **FIGURE 66**

MGSGPLVLVLLLTLLGSSHGTGPGMTLQLKLKESFLTNSSESSFLELLEKLCLLLHLPSTSVTL  
HHARSQHHVVCNT

**Important features:**

**Signal peptide:**

amino acids 1-19

**N-glycosylation site.**

amino acids 37-41

**N-myristoylation sites.**

amino acids 15-21, 19-25, 60-66

## FIGURE 67

ACGGACCGAGGGTTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCGGGC  
CAGGTGCCCCGTGCGCAGGTGCCCCTGCCCGGAGATGCGGTAGGAGGGGCGAGCGCGAGAAGCCCC  
TTCCTCGGCGCTGCCAACCCGCCACCCAGCCCATGGCGAACCCCGGGCTGGGGCTGCTTCTGGCG  
CTGGGCCTGCCGTTCTTGCTGGCCCGCTGGGGCCGAGCCTGGGGGCAAATACAGACCACTTCTGC  
AAATGAGAAATAGCACTGTTTTGCCCTTCATCCACCAGCTCCAGCTCCGATGGCAACCTGCGTCCGG  
AAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGGCTGCCTTGCTCCTGGCTGTGGGGCTG  
GCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGGCACCTACCGGCCAGTAGCGA  
GGAGCAGTTCTCCCATGCAGCCGAGGCCCGGGCCCCCTCAGGACTCCAAGGAGACGGTGCAGGGCT  
GCCTGCCCATCTAGGTCCCCCTCTCCTGCATCTGTCTCCCTTCATTGCTGTGTGACCTTGGGGAAA  
GGCAGTGCCCTCTCTGGGCAGTCAGATCCACCCAGTGCTTAATAGCAGGGAAGAAGGTACTTCAA  
AGACTCTGCCCCCTGAGGTCAAGAGAGGATGGGGCTATTCACTTTTATATATTTATATAAAATTAG  
TAGTGAGATGTAAAAAAAAAAAAAAAAAAAA

## **FIGURE 68**

MANPGLGLLLALGLPFLRLRWGRAWGQIQTTSANENSTVLPSTSSSSDGNLRPEAITAIIVVFS  
LLAALLLAVGLALLVRKLREKRQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

### **Important features:**

#### **Signal peptide:**

amino acids 1-19

#### **Transmembrane domain:**

amino acids 56-80

#### **N-glycosylation site.**

amino acids 36-40

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 86-90

#### **Tyrosine kinase phosphorylation site.**

amino acids 86-94

#### **N-myristoylation sites.**

amino acids 7-13, 26-32

## FIGURE 69

GCCAGGAATAACTAGAGAGGAACAATGGGGTTATTAGAGGTTTTGTTTTCTCTTAGTTCTGTGCCTGCTGCACCAG  
TCAAATACTTCTCTTATTAAGCTGAATAATAATGGCTTTGAAGATATTGTCATTGTTATAGATCCTAGTGTGCCAGAA  
GATGAAAAAATAATGAACAAATAGAGGATATGGTGACTACAGCTTCTACGTACCTGTTTGAAGCCACAGAAAAAGA  
TTTTTTTTCAAAAATGTATCTATATTAATTCCTGAGAATTGGAAGGAAATCCTCAGTACAAAAGGCCAAAACATGAA  
AACCATAAACATGCTGATGTTATAGTTGCACCACCTACACTCCCAGGTAGAGATGAACCATACACCAAGCAGTTCCACA  
GAATGTGGAGAGAAAGGCCGAATACATTCACCTTCCACCTTCTACTTGGAAAAAACAAAATGAATATGGACCA  
CCAGGCAAACTGTTTGTCCATGAGTGGGCTCACCTCCGGTGGGGAGTGTTTGTAGTACATGAAGATCAGCCTTTC  
TACCGTGCTAAGTCAAAAAAATCGAAGCAACAAGGTGTTCCGCAGGTATCTCTGGTAGAATAGAGTTTATAAGTGT  
CAAGGAGGCAGCTGCTTAGTAGAGCATGCAGAATTGATTCTACAACAAAACCTGTATGGAAAAGATTGTCAATTCCTT  
CCTGATAAAGTACAACAGAAAAAGCATCCATAATGTTTATGCAAAGTATTGATTCTGTTGTTGAATTTGTAAACGAA  
AAAACCCATAATCAAGAAGCTCCAAGCCTACAAAACATAAAGTGCAATTTTAGAAGTACATGGGAGGTGATTAGCAAT  
TCTGAGGATTTTAAAAACACCATACCCATGGTGACACCACCTCCTCCACCTGTCTTCTCATGTCTGAAGATCAGTCAA  
AGAATTGTGTGCTTAGTTCTTGTATAAGTCTGGAAGCATGGGGGTAAGGACCGCCTAAATCGAATGAATCAAGCAGCA  
AAACATTTCTGCTGCAGACTGTTGAAAATGGATCCTGGGTGGGGATGGTTCACTTTGATAGTACTGCCACTATTGTA  
AATAAGCTAATCCAAATAAAAGCAGTGATGAAAGAAACACACTCATGGCAGGATTACCTACATATCCTCTGGGAGGA  
ACTTCCATCTGCTCTGGAATTAATATGCATTTCAAGGTGATTGGAGAGTACATTCCTCAACTCGATGGATCCGAAGTA  
CTGCTGCTGACTGATGGGGAGGATAACACTGCAAGTCTTGTATTGATGAAGTGAACAAAAGTGGGGCCATTGTTTAT  
TTTATTGCTTTGGGAAGAGTGTGATGAAGCAGTAATAGAGATGAGCAAGATAACAGGAGGAAGTCATTTTATGTT  
TCAGATGAAGCTCAGAACATGGCCTCATTGATGCTTTTGGGGCTCTTACATCAGGAAATACTGATCTCTCCGAGAAG  
TCCCTTCAGCTCGAAAGTAAGGGATTAACTGTAATAGTAAATGCCTGGATGAACGACACTGTCATAATTGATAGTACA  
GTGGGAAAGGACAGTCTTCTCATCACATGGAACAGTCTGCCTCCAGTATTCTCTCTGGGATCCAGTGGGAACA  
ATAATGGAAAAATTCAGTGGATGCAACTTCCAAAATGGCCTATCTCAGTATTCCAGGAACGCAAGGTGGGCACT  
TGGGCATACAATCTTCAAGCCAAAGCGAACCCAGAAACATTAACATTTACAGTAACCTTCTCGAGCAGCAAATCTTCT  
GTGCCTCCAATCACAGTGAATGCTAAATGAATAAGGACGTAACAGTTCCTCCAGCCCAATGATTGTTTACGCAGAA  
ATTCTACAAGGATATGTACCTGTTCTTGGAGCCAATGTGACTGCTTTCATTGAATCACAGAATGGACATACAGAAGTT  
TTGGAACCTTTGGATAATGGTGCAGGCGCTGATTCTTCAAGAATGATGGAGTCTACTCCAGGTATTTTACAGCATAT  
ACAGAAAATGGCAGATATAGCTTAAAAGTTCGGGCTCATGGAGGAGCAACACTGCCAGGCTAAAATTACGGCCTCCA  
CTGAATAGAGCCGCTACATACCAGGCTGGGTAGTGAACGGGGAAATTAAGCAAAACCCGCCAAGACCTGAAATTTGAT  
GAGGATACTCAGACCACCTTGGAGGATTTCAAGCGAACAGCATCCGGAGGTGCATTTGTGGTATCACAAAGTCCCAAGC  
CTTCCCTTGCCCTGACCAATACCCCAAGTCAAATCACAGACCTTGATGCCACAGTTTATGAGGATAAGATTATTCTT  
ACATGGACAGCACCAGGAGATAATTTTATGTTGGAAAAGTTCAACGTTATATCATAAGAAATAGTGCAAGTATTCTT  
GATCTAAGAGACAGTTTTGATGATGCTCTTCAAGTAAATACTACTGATCTGTCCACCAAGGAGGCCAACTCCAAGGAA  
AGCTTTGCAATTTAAACCAGAAAATATCTCAGAAGAAAATGCAACCCACATATTTTATGCCATTAAAGTATAGATAAA  
AGCAATTTGACATCAAAAGTATCCAACATTGCACAAGTAACTTTGTTTATCCCTCAAGCAAAATCCTGATGACATTGAT  
CCTACACCTACTCCTACTCCTACTCCTACTCCTGATAAAAGTCATAATTTCTGGAGTTAATATTTCTACGCTGGTATTG  
TCTGTGATTGGGTCTGTTGTAATTTGTTAACTTTATTTTAAGTACCACCATTTGAACCTTAACGAAGAAAAAATCTTC  
AAGTAGACCTAGAAGAGAGTTTTAAAAAACAAAACAAATGTAAGTAAAGGATATTTCTGAATCTTAAATTCATCCCAT  
GTGTGATCATAAACTCATAAAAATAATTTTAAGATGTGCGAAAAGGATACCTTTGATTAAATAAAAAACACTCATGGATA  
TGTA AAAACTGTCAAGATTAATTTAATAGTTTCATTTATTTGTTATTTTATTGTAAGAAATAGTGATGAACAAAG  
ATCCTTTTTCATACTGATACCTGGTTGTATATTATTTGATGCAACAGTTTCTGAAATGATATTTCAAATTCATCAA  
GAAATTAATATCATCTATCTGAGTAGTCAAAATACAAGTAAAGGAGAGCAAAATAAACACATTTGGAAAAA  
AA

## **FIGURE 70**

MGLFRGFVFLVLCLLHQSNSTSFIKLNNNGFEDIVIVIDPSVPEDEKIEQIEDMVTASTYLFE  
ATEKRFFFKNVSILIPENWKENPQYKRPKHENHKHADVIVAPPTLPGRDEPYTKQFTECGEKGEY  
IHFTPDLLLGGKKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATRCISAGISGRN  
RVYKCQGGSCLSRACRIDSTTKLYGKDCQFFPDQVQTEKASIMFMQSIDSVEFCNEKTHNQEAP  
SLQNIKCNFRSTWEVISNSEDFKNTIPMVTPPPPVFSLLKISQRIVCLVLDKSGSMGGKDRLNR  
MNQAAKHFLQLQTVENGSWVGMVHFDSTATIVNKLIQIKSSDERNTLMAGLPTYPLGGTSICSGIK  
YAFQVIGELHSQLDQSEVLLLTGDNNTASSCIDEVKQSGAIVHFIALGRAADEAVIEMSKITGG  
SHFYVSDEAQNGLIDAFGALTSGNTDLSQKSLQLESKGLTLNSNAWMNDTVIIDSTVGKDTFFL  
ITWNSLPPSISLWDPSGTIMENFTVDATSKMAYLSIPGTAKVGTWAYNLQAKANPETLTITVTSR  
AANSSVPPITVNAKMKNKDVNSFPSPMIVYAEILQGYVPVLGANVTAFIESQNGHTEVLELLDNGA  
GADSFKNQGVYSRYFTAYTENGRYSLKVRAHGGANTARLKLRPPLNRAAYIPGWVNGEIEANPP  
RPEIDEDTQTLEDTSRTASGGAFVVSQVPSLPLPDQYPPSQITDLDTVHEDKIIILTWTAPGDN  
FDVGKVQRYIIRISASILDLRDSFDDALQVNTTDLSPKEANSKESFAFKPENISEENATHIFIAI  
KSIDKSNLTSKVSANIAQVTLFIPQANPDDIDPTPTPTPTPTPKSHNSGVNISTLVLSVIGSVVI  
VNFILSTTI

### **Signal peptide:**

amino acids 1-21

### **Putative transmembrane domains:**

amino acids 284-300, 617-633

### **Leucine zipper pattern.**

amino acids 469-491, 476-498

### **N-glycosylation site.**

amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,  
628-632, 811-815, 832-836, 837-841, 852-856, 896-900

## FIGURE 71

CTCCTTAGGTGGAAACCTGGGAGTAGAGTACTGACAGCAAAGACCGGGAAAGACCATACGTCCCGGGGAGGGGTGA  
CAACAGGTGTCTATCTTTTGTATCTCGTGTGTGGCTGCCTTCTTATTTCAAGGAAAGACGCCAAGTAATTTTGACCCA  
GAGGAGCAATGATGTAGCCACCTCCTAACCTTCCCTTCTTGAACCCCAAGTTATGCCAGGATTTACTAGAGAGTGTCA  
ACTCAACCAGCAAGCGGCTCCTTCGGCTTAACCTTGTGGTTGGAGGAGAGAACCTTTGTGGGGCTGCCTTCTCTAGCA  
GTGCTCAGAAGTGACTTGCCTGAGGGTGGACCAAGAAAGGAAAGGTCCCTCTTGTCTGTGGCTGCACATCAGGAA  
GGCTGTGATGGGAATGAAGGTGAAACTTGGAGATTTCACTTCAGTCATTGCTTCTGCCTGCAAGATCATCTTTAAA  
AGTAGAGAAGCTGCTCTGTGTGGTGGTTAACTCCAAGAGGCAGAACTCGTCTTAGAAGGAAATGGATGCAAGCAGCTC  
CGGGGGCCCCAACGCATGCTTCTGTGGTCTAGCCCAGGGAAGCCCTTCCGTGGGGGGCCCCGGCTTTGAGGGATGCC  
ACCGGTTCTGGACGCATGGCTGATCTCTGAATGATGATGGTTCCGCCGGGGGCTGCTTGCCTGGATTTCGCCGGTGGTG  
GTTTTGTGGTGTCTCTGTGTGTCTATCTCTGTCTGTACATGTTGGCTGCACCCCAAGGTGACGAGGAGCAG  
CTGGCACTGCCAGGGCCAAACGCCCCACGGGGAAGGAGGGGTACCAGGCCGTCTTCAGGAGTGGGAGGAGCAGCAC  
CGCAACTACGTGAGCAGCCTGAAGCGGCAGATCGCACAGCTCAAGGAGGAGCTGCAGGAGAGGAGTGAGCAGCTCAGG  
AATGGGCACTCAACAGCCAGCGATGCTGTCTGGCTGGGTCTGGACAGGAGCCCCCAGAGAAAACCCAGGCCGACCTC  
CTGGCCTTCTCTGACTCGCAGGTGGACAAGGCAGAGGTGAATGCTGGCTCAAGCTGGCCACAGAGTATGCAGCAGTG  
CCTTTCGATAGCTTTACTCTACAGAAGGTGTACCAGCTGGAGACTGGCCTTACCCGCCACCCCGAGGAGAAGCCTGTG  
AGGAAGGACAAGCGGGATGAGTTGGTGGAAAGCCATTGAATCAGCCTTGGAGACCCTGAACAACTCTGCAGAGAACAGC  
CCCAATCACCGTCTTACACGGCTCTGATTTATAGAAGGGATCTACCGAACAGAAAGGGACAAAGGGACATTGTAT  
GAGCTCACCTTCAAAGGGGACCAAAACACGAATTCAAACGGCTCATCTTATTTGACCACTTCAGCCCCATCATGAAA  
GTGAAAAATGAAAAGCTCAACATGGCCAAACAGCTTATCAATGTTATCTGCTCTAGCAAAAAGGGTGGACAAGTTC  
CGGCAGTTCATGCAGAAATTCAGGGAGATGTGCATTGAGCAGGATGGGAGAGTCCATCTCACTGTTGTTTACTTTGGG  
AAAGAAGAAATAAATGAAGTCAAGGAATACTTGAACACACTTCCAAGCTGCCAACTTCAGGAACCTTACCTTCATC  
CAGCTGAATGGAGAATTTCTCGGGGAAGGGACTTGATGTTGGAGCCCGCTTCTGGAAGGAAGCAACGTCCTTCTC  
TTTTTCTGTGATGTGGACATCTACTTACATCTGAATTCCTCAATACGTGTAGGCTGAATACACAGCCAGGGGAAGAAG  
GTATTTTATCCAGTCTTTTTCAGTCAGTACAATCTGGCATAATATACGGCCACCATGATGCAGTCCCTCCCTTGGAA  
CAGCAGCTGGTCATAAAGAAAGAACTGGATTTTGGAGAGACTTTGGATTGGGATGACGTGTCACTATCGGTTCAGAC  
TTTCATCAATATAGGTGGGTTTGTCTGGACATCAAAGGCTGGGGCGGAGAGGATGTGCACCTTTATCGCAAGTATCTC  
CACAGCAACCTCATAGTGGTACGGACGCTGTGCGAGGACTCTTCCACCTCTGGCATGAGAAGCGCTGCATGGACGAG  
CTGACCCCGAGCAGTACAAGATGTGCATGCACTCCAAGGCCATGAACGAGGCATCCCACGGCCAGCTGGGCATGCTG  
GTGTTTCAGGCACGAGATAGAGCTCACCTTCGCAACAGAAACAGAAAGCAAGTAGCAAAAAAACAATGAAGTCCCA  
GAAGGATTGTGGGAGACACTTTTCTTTTCTTTTCAATTAAGTGGCTGCAACAGAGAAAAGACTTCCATAAA  
GGACGACAAAAGAAATGGACTGATGGGTGAGAGATGAGAAAGCCTCCGATTCTCTCTGTTGGGCTTTTACACAGA  
AATCAAAATCTCCGCTTGGCTGCAAAAGTAACCCAGTTGCACCCCTGTGAAGTGTCTGACAAAGGCAGAAATGCTTGTG  
AGATTATAAGCCTAATGGTGTGGAGGTTTGTGTTGTTTACAATACACTGAGACCTGTTGTTTGTGTGCTCATTGA  
AATATTCTAGATTAAAGAGCAGTTTGTAAAAAATTCATTAGCATGAAAGGCAAGCATATTTCTCCTCATATGAATGA  
GCCTATCAGCAGGCTCTAGTTTCTAGGAATGCTAAAAATCAGAAGGCAGGAGAGGATAGGCTTATTATGATACT  
AGTGAGTACATTAAAGTAAAAATAAATGGACCAGAAAAGAAAAGAAACCATAAATATCGTGTCAATTTTCCCAAGAT  
TAACCAAAAATAATCTGCTTATCTTTTGGTGTCTCTTTAACTGTCTCCGTTTTTTCTTTTATTTAAAAATGCACT  
TTTTTTCCCTTGTGAGTTATAGTCTGCTTATTTAATTACCACTTTGCAAGCCTTACAAGAGAGCACAAGTTGGCCTAC  
ATTTTTATATTTTTTAAGAAGATACTTTGAGATGCATTATGAGAATTTTCAGTTCAAAGCATCAAATGATGCCATAT  
CCAAGGACATGCCAAATGCTGATTCTGTGAGGCACTGAATGTGAGGCACTGAGACATAGGGAAGGAATGGTTTGTACT  
AATACAGACGTACAGATACTTCTCTGAAGATATTTTCGAAGAGGAGCAACTGAACACTGGAGGAAAAGAAAATGAC  
ACTTTCTGCTTTACAGAAAAGGAAACTCATTGAGACTGGTGATATCGTGATGTACCTAAAAGTCAGAAAACCAATTTT  
CTCCTCAGAAAGTAGGACCGCTTTCTTACCTGTTTAAATAAACCAAGTATACCGTGTGAACCAACAATCTCTTTTC  
AAAACAGGGTGCTCCTCCTGGCTTCTGGCTTCCATAAGAAGAAATGGAGAAAAATATATATATATATATATATTTGT  
GAAAGATCAATCCATCTGCCAGAATCTAGTGGGATGGAAGTTTTTGTACATGTATCCACCCAGGCCAGGTGGAAG  
TAAGTGAATATTTTTTAAATTAAGCAGTTCTACTCAATCACCAGATGCTTCTGAAAATTCATTTTATACCATTT  
CAAACTATTTTTTAAAAATAAATACAGTTAATAGAGTGGTTTCTTCATTATGTGAAAATTTATTAGCCAGCACCAG  
ATGCATGAGCTAATTATCTCTTGAAGTCTTGTCTGTTTGTCTCAGAGTAACTCATTGTTTAAAGCTTCAAGAAC  
ATTCAAGCTGTTGGTGTGTTAAAAATGCATTGTATTGATTGTACTGGTAGTTTAAATTAATTAACACAGG  
CCATGAATGGAAGGTGGTATTGCACAGCTAATAAAATATGATTTGTGGATATGAA

## **FIGURE 72**

MMMVRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQLALPRANSPTGKEGYQAVLQEW  
EQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFLHSQV  
AEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPEEKPVKDKRDELVEAIESALETLNPA  
ENSPNHRPYTASDFIEGIYRTERDKGTLIELTFKGDHKHEFKRLILFRPFSPIMKVNEKLNMA  
TLINIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVGILENTSKAANFRNF  
TFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNLCRLNTQPGKKVFYPVLSQY  
NPGIIYGHHDVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFINIGGFLLDIKGWGGEDVHLYR  
KYLHSNLIIVRTPVRGLFHLWHEKRCMDLTPEQYKMCQSKAMNEASHGQLGMLVFRHEIEAHL  
RKQKQKTSSKKT

### **Important features:**

#### **Signal peptide:**

amino acids 1-27

#### **N-glycosylation sites.**

amino acids 315-319, 324-328

#### **N-myristoylation sites.**

amino acids 96-102, 136-142, 212-218, 311-317, 339-345, 393-399

#### **Amidation site.**

amino acids 377-381



[illegible][illegible]

## **FIGURE 74**

MLFSALLEVIWILAADGGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTFDPDLPALQ  
PHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPGSEHQINSEAT  
FAELHIVHYSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPP  
FNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLGTLFSTEEEPSKLLV  
QNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVYFIARKIRKKRLENRKS  
VVFTSAQATTEA

**Important features of the protein:**

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 291-310

**N-glycosylation site.**

amino acids 213-216

**Eukaryotic-type carbonic anhydrases proteins**

amino acids 197-245, 104-140, 22-69

## FIGURE 75

TGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCGCCTTGGGGACGGGCAGTTCCTGTGTC  
TCTGGTGGTTTGCCTAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGAATGTCCTACA  
ATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATTTTCATCACAA  
ATTGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTCTGTGTCTGACAGCTCC  
AGAGAAGTGAAGAGAAATCCAGAAGACCTTCTGTTTCCATGCAACAAATATACTCCAATCTGA  
AGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCCAGTGTGTGACCAACCAC  
ACGCTGGTGCTCACCTGGCTGGAGCCGAACACTCTTTACTGCGTACACGTGGAGTCCTTCGTCCC  
AGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTGCCAGGACTTTGAAAGATCAATCAT  
CAGAGTTCAAGGCTAAAATCATCTTCTGGTATGTTTTGCCCATATCTATTACCGTGTTCCTTTTT  
TCTGTGATGGGCTATTCCATCTACCGATATATCCACGTGGCAAAGAGAAACACCCAGCAAATTT  
GATTTTGATTTATGGAAATGAATTTGACAAAAGATTCTTTGTGCCTGCTGAAAAATCGTGATTA  
ACTTTATCACCTCAATATCTCGGATGATTCTAAAATTTCTCATCAGGATATGAGTTTACTGGGA  
AAAAGCAGTGATGTATCCAGCCTTAATGATCCTCAGCCCAGCGGGAACCTGAGGCCCCCTCAGGA  
GGAAGAGGAGGTGAAACATTTAGGGTATGCTTCGCATTTGATGGAATTTTTTGTGACTCTGAAG  
AAAAACGGAAGGTACTTCTCTACCCAGCAAGAGTCCCTCAGCAGAACAATACCCCGGATAAA  
ACAGTCATTGAATATGAATATGATGTGAGAACCCTGACATTTGTGCGGGGCCTGAAGAGCAGGA  
GCTCAGTTTGCAAGGAGGAGGTGTCCACACAAGGAACATTATTGGAGTCGAGGCAGCGTTGGCAG  
TCTTGGGCCCCGAAACGTTACAGTACTCATACCCCCTCAGCTCCAAGACTTAGACCCCCTGGCG  
CAGGAGCACACAGACTCGGAGGAGGGGCCGAGGAAGAGCCATCGACGACCCTGGTCGACTGGGA  
TCCCCAACTGGCAGGCTGTGTATTCTTCGCTGTCCAGCTTCGACCAGGATTCAGAGGGCTGCG  
AGCCTTCTGAGGGGGATGGGCTCGGAGAGGAGGGTCTTCTATCTAGACTCTATGAGGAGCCGGCT  
CCAGACAGGCCACCAGGAGAAAATGAAACCTATCTCATGCAATTCATGGAGGAATGGGGTTATA  
TGTGCAGATGGAAAACTGATGCCAACCTTCCTTTTGCTTTTGTTCCTGTGCAACAAGTGAG  
TCACCCCTTTGATCCCAGCCATAAAGTACCTGGGATGAAAGAAGTTTTTCCAGTTTGTGAGTGT  
CTGTGAGAATTACTTATTTCTTTTCTCTATTCTCATAGCACGTGTGTGATTGGTTCATGCATGTA  
GGTCTCTTAACAATGATGGTGGGCCTCTGGAGTCCAGGGGCTGGCCGGTTGTTCTATGCAGAGAA  
AGCAGTCAATAAATGTTTGCCAGACTGGGTGCAGAATTTATTCAGGTGGGTGT

## **FIGURE 76**

MSYNGLHQRVFKELKLLTLCSSISQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIY  
SNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSEKQCARTLK  
DQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRYIHVGKEKHPANLILYGNEDKRFFVPAEK  
IVINFITLNISSDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKHLGYASHLMEIFC  
DSEENTEGTSLTQQESLSRTIPDKTVIEYEYDVRTTDCAGPEEQELSLQEEVSTQGTLLESQA  
ALAVLGPQTLQYSYTPQLQDLPLAQEHTDSEEGPEEEPSTTLVDWDPQTGRLCIPSLSSFDQDS  
EGCEPSEGDGLGEEGLLSRLYEPPAPDRPPGENETYLMQFMEEWGLYVQMEN

### **Important features:**

#### **Signal peptide:**

amino acids 1-28

#### **Transmembrane domain:**

amino acids 140-163

#### **N-glycosylation sites.**

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

## FIGURE 77

GAGGAGCGGGCCGAGGACTCCAGCGTGCCCGAGGTCTGGCATCCTGCACCTTGCTGCCCTCTGACAC  
CTGGGAAGATGGCCCGCCCGTGGACCTTCACCCCTCTCTGTGGTTTGCTGGCAGCCACCTTGATC  
CAAGCCACCTCAGTCCCACTGCAGTTCTCATCCTCGGCCAAAAGTCATCAAAGAAAAGCTGAC  
ACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGCTCAGTGCCATGC  
GGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGGCAGCCTGGTGAACACCGTCTGAAGCACATC  
ATCTGGCTGAAGGTGATCACAGCTAACATCCTCCAGCTGCAGGTGAAGCCCTCGGCCAATGACCA  
GGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCAACACGCCCCCTGGTCAAGACCA  
TCGTGGAGTTCCACATGACGACTGAGGCCCAAGCCACCATCCGCATGGACACCAGTGCAAGTGGC  
CCCCACCGCCTGGTCTCAGTGACTGTGCCACCAGCCATGGGAGCCTGCGCATCCAAGTCTGTGA  
TAAGCTCTCCTTCCTGGTGAACGCCTTAGCTAAGCAGGTGATGAACCTCCTAGTGCCATCCCTGC  
CCAATCTAGTGAAAAACCAGCTGTGTCCCGTGATCGAGGCTTCCTTCAATGGCATGTATGCAGAC  
CTCCTGCAGCTGGTGAAGGTGCCCATTTCCCTCAGCATTGACCGTCTGGAGTTTGACCTTCTGTGA  
TCCTGCCATCAAGGGTGACACCATTACAGCTCTACCTGGGGGCCAAGTTGTTGGACTCACAGGGAA  
AGGTGACCAAGTGGTTCAATAACTCTGCAGCTTCCCTGACAATGCCACCCTGGACAACATCCCG  
TTCAGCCTCATCGTGAGTCAGGACGTGGTGAAAGCTGCAGTGGCTGCTGTGCTCTCTCCAGAAGA  
ATTCATGGTCTGTTGGACTCTGTGCTTCCCTGAGAGTGCCCATCGGCTGAAGTCAAGCATCGGGC  
TGATCAATGAAAAGGCTGCAGATAAGCTGGGATCTACCCAGATCGTGAAGATCCTAACTCAGGAC  
ACTCCCGAGTTTTTTATAGACCAAGGCCATGCCAAGGTGGCCCAACTGATCGTGCTGGAAGTGT  
TCCCTCCAGTGAAGCCCTCCGCCCTTTGTTACCCCTGGGCATCGAAGCCAGCTCGGAAGCTCAGT  
TTTACACCAAAGGTGACCAACTTATACTCAACTTGAATAACATCAGCTCTGATCGGATCCAGCTG  
ATGAACTCTGGGATTGGCTGGTTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCCA  
CTCCATCCTGCTGCCGAACCAGAATGGCAAATTAAGATCTGGGGTCCCAGTGTCATTGGTGAAGG  
CCTTGGGATTGAGGCAGCTGAGTCCTCACTGACCAAGGATGCCCTTGTGCTTACTCCAGCCTCC  
TTGTGGAAACCCAGCTCTCCTGTCTCCAGTGAAGACTTGATGGCAGCCATCAGGGAAGGCTGG  
GTCCCAGCTGGGAGTATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAATCAATAAACTTG  
CCTGTGAAAAA

## **FIGURE 78**

MAGPWTFLLCGLLAATLIQATLSPTAVLILGPKVKEKLTQELKDHNATSILQQLPLLSAMREK  
PAGGIPVLGSLVNTVLKHI IWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPLVKTIVE  
FHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMNLLVPSLPNL  
VKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYP AIKGDTIQLYLGAKLLDSQGKVT  
KWFNNSAASLTMP TLDNIPFSLIVSQDVVKA AVAVLSPEEFMVLLDSVLPESAHLKSSIGLIN  
EKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSSEALRPLFTLGLIEASSEAQFYT  
KGDQLILNLNNISSDRIQLMNSGIGWFQPDVLKNIITEIIHSILLPNQNGKLRS GVPVSLVKALG  
FEAAESSLT KDALVLT PASLWKPPSPVSQ

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-21

#### **N-glycosylation sites.**

amino acids 48-51, 264-267, 401-404

#### **Glycosaminoglycan attachment site.**

amino acids 412-415

#### **LBP / BPI / CETP family proteins.**

amino acids 407-457

## FIGURE 79

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAGAGC  
TTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCCATGGCCTCT  
CTTGGCCTCCAACCTTGTGGGCTACATCCTAGGCCTTCTGGGGCTTTGGGCACACTGGTTGCCAT  
GCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTCGGTGCCAGCATTGTGACAGCAGTTGGCTTCT  
CCAAGGGCCTCTGGATGGAATGTGCCACACAGCACAGGCATCACCCAGTGTGACATCTATAGC  
ACCCCTTCTGGGCCTGCCCGCTGACATCCAGGCTGCCAGGCCATGATGGTGACATCCAGTGCAAT  
CTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCACAGTCTTCTGCCAGGAATCCC  
GAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTCATCCTTGGAGGCCTCCTGGGATTC  
ATTCTGTGGCTGGAATCTTCATGGGATCTACGGGACTTCTACTCACCAGTGGTGCCTGACAG  
CATGAAATTTGAGATTGGAGAGGCTCTTTACTTGGGCATTATTTCTTCCCTGTTCTCCCTGATAG  
CTGGAATCATCCTCTGCTTTTCTGCTCATCCCAGAGAAATCGCTCCAATACTACGATGCCTAC  
CAAGCCCAACCTCTTGCCACAAGGAGCTCTCCAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGA  
GTTCAATTCTTACAGCCTGACAGGGTATGTGTGAAGAACCAGGGGCCAGAGCTGGGGGGTGGCTG  
GGTCTGTGAAAAACAGTGACAGCACCCCGAGGGCCACAGGTGAGGGACACTACCACTGGATCGT  
GTCAGAAGGTGCTGCTGAGGATAGACTGACTTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGG  
GCTAGTGTAACAGCATGCAGGTTGAATTGCCAAGGATGCTCGCCATGCCAGCCTTCTGTTTTCC  
TCACCTTGCTGCTCCCTGCCCCTAAGTCCCCAACCTCAACTGAAACCCCATTCCTTAAGCCA  
GGACTCAGAGGATCCCTTTGCCCTCTGGTTTACCTGGGACTCCATCCCCAACCCACTAATCACA  
TCCCACTGACTGACCCTCTGTGATCAAAGACCCTCTCTCTGGCTGAGGTTGGCTCTTAGCTCATT  
GCTGGGGATGGGAAGGAGAAGCAGTGGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTC  
CCTCCAAAGAACTGATTGGCCCTGGAACCTCCATCCCACTCTTGTATGACTCCACAGTGTCCA  
GACTAATTTGTGCATGAACGAAATAAAACCATCTACGGTATCCAGGGAACAGAAAGCAGGATG  
CAGGATGGGAGGACAGGAAGGCAGCCTGGGACATTTAAAAAATA

## **FIGURE 8o**

MASLGLQLVGYYLGLLGLLGLTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGITQCD  
IYSTLLGLPADIQAAQAMMTSSAIISSLACIISVVGMRCTVFCQESRAKDRVAVAGGVFFILGGL  
LGFIPVAWNLHGILRDFYSPLVPDSMKFEIGEALYLGIISSLSLIAGIILCFSCSSQRNRSNYY  
DAYQAQPLATRSSPRPGQPPKVKSEFNYSYSLTGYV

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-24

#### **Transmembrane domains:**

amino acids 82-102, 117-140, 163-182

#### **N-glycosylation site.**

amino acids 190-193

#### **PMP-22 / EMP / MP20 family proteins.**

amino acids 46-59



## FIGURE 81

CCCACGCGTCCGCGCCTCTCCCTTCTGCTGGACCTTCCTTCGTCTCTCCATCTCTCCCTCCTTTC  
CCCGCGTTCTCTTTCCACCTTTCTCTTCTTCCCACCTTAGACCTCCCTTCCTGCCCTCCTTTCCCT  
GCCCACGCTGCTTCTTGCCCTTCTCCGACCCGCTCTAGCAGCAGACCTCCTGGGGTCTGTGG  
GTTGATCTGTGGCCCTGTGCCTCCGTGTCCTTTTCGTCTCCCTTCCTCCCGACTCCGCTCCCGG  
ACCAGCGGCCTGACCCTGGGGAAGGATGGTTCCCGAGGTGAGGGTCCTCTCCTCCTTGCTGGGA  
CTCGCGCTGCTCTGGTTCCCCCTGGACTCCCACGCTCGAGCCCGCCAGACATGTTCTGCCTTTT  
CCATGGGAAGAGATACTCCCCGGCGAGAGCTGGCACCCCTACTTGAGCCACAAGGCCTGATGT  
ACTGCCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGTTGTTACCGCCTCCACTGTCCGCCT  
GTCCACTGCCCCAGCCTGTGACGGAGCCACAGCAATGCTGTCCCAAGTGTGTGGAACCTCACAC  
TCCCTCTGGACTCCGGGCCCCACCAAAGTCCTGCCAGCACAACGGGACCATGTACCAACACGGAG  
AGATCTTCAGTGCCCATGAGCTGTTCCCTCCCGCCTGCCCAACCAGTGTGTCTCTGCAGCTGC  
ACAGAGGGCCAGATCTACTGCGGCCTCACAACCTGCCCCGAACCAGGCTGCCCAGCACCCCTCCC  
ACTGCCAGACTCCTGCTGCCAAGCCTGCAAAGATGAGGCAAGTGAAGCAATCGGATGAAGAGGACA  
GTGTGCAGTCGCTCCATGGGGTGAGACATCCTCAGGATCCATGTTCCAGTGATGCTGGGAGAAAG  
AGAGGCCCCGGGCACCCCAAGCCCCACTGGCCTCAGCGCCCCTCTGAGCTTCATCCCTCGCCACTT  
CAGACCCAAGGGAGCAGGCAGCACAACCTGTCAAGATCGTCCTGAAGGAGAAACATAAGAAAGCCT  
GTGTGCATGGCGGGAAGACGTACTCCACGGGGAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGC  
CCCTTGCCCTGCATCCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCC  
CACCAGTACCCCTGCCGTACCCCGAGAAAGTGGCTGGGAAGTGTGCAAGATTTGCCCAGAGG  
ACAAAGCAGACCCTGGCCACAGTGAGATCAGTTCTACCAGGTGTCCAAGGCACCGGGCCGGGTC  
CTCGTCCACACATCGGTATCCCCAAGCCCAGACAACCTGCGTCGCTTTGCCCTGGAACACGAGGC  
CTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAAGATGAGGAACTGAGGCTCAGAGAG  
GTGAAGTACCTGGCCCAAGGCCACACAGCCAGAATCTTCCACTTGACTCAGATCAAGAAAGTCAG  
GAAGCAAGACTTCCAGAAAGAGGCACAGCACTTCCGACTGCTCGCTGGCCCCCACGAAGGTCCT  
GGAACGTCTTCCTAGCCAGACCCTGGAGCTGAAGGTCACGGCCAGTCCAGACAAAGTGACCAAG  
ACATAACAAAGACCTAACAGTTGCAGATATGAGCTGTATAATTGTTGTTATTATATATTAATAAA  
TAAGAAGTTGCATTACCCTCAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 82**

MVPEVRVLSSLLGLALLWFPLDSHARARPDMFCLFHGKRYSPGESWHYPYLEPQGLMYCLRCTCSE  
GAHVSCYRLHCPPVHCPQPVTEPQQCCPKCVEPHTPSGLRAPPKSCQHNGTMYQHGEIFSAHELF  
PSRLPNQCVLCSCTEGQIYCGLTTCPEPGCPAPLPLPDSCCQACKDEASEQSDEEDSVQSLHGVR  
HPQDPCSSDAGRKRGPPTAPTGLSAPLSFIPRHFRPKGAGSTTVKIVLKEKHKKACVHGGKTYS  
HGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPTTEYPCRHPEKVAGKCKICPEDKADPGHSE  
ISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKLVKDEETEAQRGEVPGPRPH  
SQNLPLDSDQESQEARLPERGTALPTARWPARRSLERLPSPDPGAEGHGQSRQSDQDITKT

**Signal peptide:**

amino acids 1-25

## FIGURE 83

GACAGCTGTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTTGCCCTCCGCTCACGCAGAGCCTCTCC  
GTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCCTTCTCTCTAATCCATCCGTCACCTCTCCTGTCA  
TCCGTTTCCATGCCGTGAGGTCCATTACAGAACACATCCATGGCTCTCATGCTCAGTTTGGTTCTGAGTC  
TCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTGGGCCAGACAAGCCTGTCCAGGCCTTGGTGGGGGAG  
GACGCAGCATTCTCCTGTTTCTGTCTCCTAAGACCAATGCAGAGGCCATGGAAGTGCAGTTTCTCAGGGG  
CCAGTTCTCTAGCGTGGTCCACCTCTACAGGGACGGGAAGGACCAGCCATTTATGCAGATGCCACAGTATC  
AAGGCAGGACAAAACCTGGTGAAGGATTCTATTGCGGAGGGGCGCATCTCTCTGAGGCTGGAAAACATTACT  
GTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCCAGTCTTACTACCAGAAGGCCATCTGGGAGCT  
ACAGGTGTGAGCACTGGGCTCAGTTTCTCTCATTTCATCACGGGATATGTTGATAGAGACATCCAGCTAC  
TCTGTGAGTCTCGGGCTGGTTCCCCCGGCCACAGCGAAGTGGAAGTCCACAAGGACAGGATTGTGCC  
ACAGACTCCAGGACAAACAGAGACATGCATGGCCTGTTTGATGTGGAGATCTCTCTGACCGTCCAAGAGAA  
CGCCGGGAGCATATCCTGTTCCATGCGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAG  
GAGATACCTTTTTCGAGCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGAATACTCTGCTGTGGCCTA  
TTTTTTGGCATTGTTGGACTGAAGATTTTCTTCTCCAAATTCCAGTGGAAAATCCAGGCGGAACCTGGACTG  
GAGAAGAAAGCAGCGACAGGCAGAATTGAGAGACGCCCCGAAACACGCAGTGGAGGTGACTCTGGATCCAG  
AGACGGCTCACCGAAGCTCTGCGTTTCTGATCTGAAAACCTGTAACCCATAGAAAAGCTCCCCAGGAGGTG  
CCTCACTCTGAGAAGAGATTTACAAGGAAGAGTGTGGTGGCTTCTCAGAGTTTCCAAGCAGGGAACATTA  
CTGGGAGGTGGACCGAGGACACAATAAAGGTGGCGCTGGGAGTGTGCCGGGATGATGTGGACAGGAGGA  
AGGAGTACGTGACTTTGTCTCCCGATCATGGGTACTGGGTCTCAGACTGAATGGAGAACATTTGTATTTT  
ACATTAATCCCGTTTTATCAGCGTCTTCCCCAGGACCCACCTACAAAATAGGGGTCTTCCTGGACTA  
TGAGTGTGGGACCATCTCCTTCTCAACATAAATGACCAGTCCCTTATTTATACCCTGACATGTGGTTTG  
AAGGCTTATTGAGGCCCTACATTGAGTATCCGTCTATAATGAGCAAAATGGAACCTCCCATAGTCATCTGC  
CCAGTCACCCAGGAATCAGAGAAAGAGGCCTCTTGGCAAAGGGCCTCTGCAATCCCAGAGACAAGCAACAG  
TGAGTCTCTCTACAGGCAACCACGCCCTTCTCCCCAGGGGTGAAATGTAGGATGAATCACATCCCACAT  
TCTTCTTTAGGGATATTAAGGTCTCTCTCCAGATCCAAAGTCCCGCAGCAGCCGGCCAAGGTGGCTTCCA  
GATGAAGGGGGACTGGCCTGTCCACATGGGAGTCAGGTGTGATGGCTGCCCTGAGCTGGGAGGGAAGAAGG  
CTGACATTACATTTAGTTTGTCTCACTCCATCTGGCTAAGTGATCTTGAAATACCACCTCTCAGGTGAAG  
AACCCTCAGGAATTTCCATCTCACAGGCTGTGGTGTAGATTAAGTAGACAAGGAATGTGAATAATGCTTAG  
ATCTTATTGATGACAGAGTGTATCCTAATGGTTTGTTCATTATATTACACTTTCAGTAAAAAAA

## **FIGURE 84**

MALMLSLVLSLLKLGSGQWQVFGPDKPVQALVGEDAAFSCFLSPKTNAEAMEVRFFRGQFSSVVH  
LYRDGKDQPFMQMPQYQGRTKLVKDSIAEGRISLRLENITVLDAGLYGCRISQSYQKAIWELQ  
VSALGSVPLISITGYVDRDIQLLCQSSGWFPRTAKWKGPQGDLSTDSRTNRDMHGLFDVEISL  
TVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLFFGIVGLKIFFSK  
FQWKIQAELDWRRKHGQAEIRDARKHAVEVTLDPETAHPKLCVSDLKTVTHRKAQEVPHSEKRF  
TRKSVVASQSFQAGKHYWEVDGGHNKRWRVGVCRDDVDRRKEYVTLSPDHGYWVLRNLNGEHLYFT  
LNPRFISVFPRTPTTKIGVFLDYECGTISFFNINDQSLIYTLTCREFGLLRPYIEYPSYNEQNGT  
PIVICPVTQESEKEASWQRASAIPESTSSESSQATTPFLPRGEM

### **Signal peptide:**

amino acids 1-17

### **Transmembrane domain:**

amino acids 239-255

## FIGURE 85

AACAGACGTTCCCTCGCGGCCCTGGCACCTCTAACCCAGACATGCTGCTGCTGCTGCTGCCCCCT  
GCTCTGGGGGAGGGAGAGGGCGGAAGGACAGACAAGTAAACTGCTGACGATGCAGAGTTCCGTGA  
CGGTGCAGGAAGGCCTGTGTGTCCATGTGCCCTGCTCCTTCTCCTACCCCTCGCATGGCTGGATT  
TACCCTGGCCCAGTAGTTCATGGCTACTGGTTCCGGGAAGGGGCCAATACAGACCAGGATGCTCC  
AGTGGCCACAAACAACCCAGCTCGGGCAGTGTGGGAGGAGACTCGGGACCGATTCCACCTCCTTG  
GGGACCCACATACCAAGAATTGCACCCCTGAGCATCAGAGATGCCAGAAGAAGTGATGCGGGGAGA  
TACTTCTTTTCGTATGGAGAAAGGAAGTATAAAATGGAATTATAAACATCACCGCTCTCTGTGAA  
TGTGACAGCCTTGACCCACAGGCCCAACATCCTCATCCAGGCACCCTGGAGTCCGGCTGCCCCC  
AGAATCTGACCTGCTCTGTGCCCTGGGCCTGTGAGCAGGGGACACCCCTATGATCTCCTGGATA  
GGGACCTCCGTGTCCCCCTGGACCCCTCCACCACCCGCTCCTCGGTGCTCACCCCTCATCCACA  
GCCCCAGGACCATGGCACCAGCCTCACCTGTCAGGTGACCTTCCCTGGGGCCAGCGTGACCACGA  
ACAAGACCGTCCATCTCAACGTGTCTACCCGCCTCAGAACTTGACCATGACTGTCTTCCAAGGA  
GACGGCACAGTATCCACAGTCTTGGGAAATGGCTCATCTCTGTCACTCCAGAGGGCCAGTCTCT  
GCGCCTGGTCTGTGCAGTTGATGCAGTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGA  
GAGGCCTGACCCTGTGCCCCCTACAGCCCTCAAACCCGGGGGTGCTGGAGCTGCCTTGGGTGCAC  
CTGAGGGATGCAGCTGAATTCACCTGCAGAGCTCAGAACCCCTCTCGGCTCTCAGCAGGTCTACCT  
GAACGTCTCCCTGCAGAGCAAAGCCACATCAGGAGTGACTCAGGGGGTGGTCCGGGGAGCTGGAG  
CCACAGCCCTGGTCTTCTGTCTTCTGCGTCATCTTCGTTGTAGTGAGGTCTGCAGGAAGAAA  
TCGGCAAGGCCAGCAGCGGGCGTGGGAGATACGGGCATAGAGGATGCAAACGCTGTGAGGGGTTT  
AGCCTCTCAGGGGCCCTGACTGAACCTTGGGCAGAAGACAGTCCCCCAGACCAGCCTCCCCAG  
CTTCTGCCCCGCTCCTCAGTGGGGGAAGGAGAGCTCCAGTATGCATCCCTCAGCTTCCAGATGGTG  
AAGCCTTGGGACTCGCGGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATCCACAG  
ATGAGAAACTGCAGAGACTCACCTGATTGAGGGATCACAGCCCCTCCAGGCAAGGGAGAAGTCA  
GAGGCTGATTCTTGTAGAATTAACAGCCCTCAACGTGATGAGCTATGATAACACTATGAATTATG  
TGCAGAGTGAAAAGCACACAGGCTTTAGAGTCAAAGTATCTCAAACCTGAATCCACACTGTGCCC  
TCCCTTTTATTTTTTAACTAAAAGACAGACAAATTCCTA

## **FIGURE 86**

MLLLLLPLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFSPSHGWIYPGPVVHGYWFREG  
ANTDQDAPVATNNPARAVWEETRDRFHLGDPHTKNCTLSIRDARRSDAGRYFFRMEKGSIKWNY  
KHHRLSVNVTALTHRPNILIPGTLESGCPQNLTCSVPWACEQGTPEMISWIGTSVSPLDPSTTRS  
SVLTLIPQPQDHGTS LTCQVTFPGASVTNKT VHLNVSYPQNLTMTVFQGDGTVSTVLGNGSSL  
SLPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPSNPGVLELPWVHLRDAAEFTCRAQNP  
LGSQQVYLVNLSLQSKATSGVTQGVVGAGATALVFLSFCVIFVVVRSCRKKSARPAAGVGDGTGIE  
DANAVRG SASQGPLETPWAEDSPPDQPPASARSSVGEGLQYASLSFQMKPWDSRGQEATDTE  
YSEIKIHR

### **Signal peptide:**

amino acids 1-15

### **Transmembrane domain:**

amino acids 351-370

## FIGURE 87

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTCTGTAC  
CCAAGGAAAGTGCAGCTGAGACTCAGACAAGATTACAATGAACCAACTCAGCTTCCTGCTGTTTC  
TCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAATGGACCTGT  
TCTTCGTCTCCATCTCTGCCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCCTAGTGCATTGA  
TGGCCTGTATTTTCTCCGCACTGAGAATGGTGTATCTACCAGACCTTCTGTGACATGACCTCTG  
GGGTGGCGCTGGACCTGGTGGCCAGCGTGCATGAGAATGACATGCGTGGGAAGTGCACGGTG  
GGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCCAGAGGGGGACGGCAACTGGGC  
CAACTACAACACCTTTGGATCTGCAGAGGGCGGCCACGAGCGATGACTACAAGAACCTGGCTACT  
ACGACATCCAGGCCAAGGACCTGGGCATCTGGCACGTGCCAATAAGTCCCCATGCAGCACTGG  
AGAAACAGCTCCCTGCTGAGGTACCGCACGGACACTGGCTTCCTCCAGACACTGGGACATAATCT  
GTTTGGCATCTACCAGAAATATCCAGTGAAATATGGAGAAGGAAAGTGTGGACTGACAACGGCC  
CGGTGATCCCTGTGGTCTATGATTTTGGCGACGCCAGAAAACAGCATCTTATTACTACCCCTAT  
GGCCAGCGGAATCACTGCGGGATTTGTTTCAGTTCAGGGTATTTAATAACGAGAGAGCAGCCAA  
CGCCTTGTGTGCTGGAATGAGGGTCACCGGATGTAACACTGAGCATCACTGCATTGGTGGAGGAG  
GATACTTTCCAGAGGCCAGTCCCCAGCAGTGTGGAGATTTTCTGGTTTGGATTGGAGTGGATAT  
GGAATCATGTTGGTTACAGCAGCAGCCGTGAGATACTGAGGCAGCTGTGCTTCTATTCTATCG  
TTGAGAGTTTTGTGGGAGGGAACCCAGACCTCTCCTCCCAACCATGAGATCCCAAGGATGGAGAA  
CAACTTACCCAGTAGCTAGAATGTTAATGGCAGAAGAGAAAACAATAAATCATATTGACTCAAGA  
AAAAAA

## **FIGURE 88**

MNQLSFLLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTENGVI  
YQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANYNTFGSAEAT  
SDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGIYQKYPVKYG  
EGKCWTDNGPVI PVVYDFGDAQKTASYSPYQREFTAGFVQFRVFNNERAANALCAGMRVTGCN  
TEHHCIGGGGYFPEASPOQCDFSGFDWSGYGTHVGYSSSREITEAAVLLFYR

**Important features:**

**Signal peptide:**

amino acids 1-16

**N-glycosylation site.**

amino acids 163-167

**Glycosaminoglycan attachment sites.**

amino acids 74-78, 289-293

**N-myristoylation sites.**

amino acids 76-82, 115-121, 124-130, 253-259, 292-298



## FIGURE 89

CTAGATTTGTCGGCTTGCAGGGGAGACTTCAGGAGTCGCTGTCTCTGAACTTCCAGCCTCAGAGAC  
CGCCGCCCTTGTCCCCGAGGGCCATGGGCCGGGTCTCAGGGCTTGTGCCCTCTCGCTTCCGTGACG  
CTCCTGGCGCATCTGGTGGTCGTCATCACCTTATTCTGGTCCCGGGACAGCAACATACAGGCCTG  
CCTGCCTCTCACGTTACCCCCGAGGAGTATGACAAGCAGGACATTCAGCTGGTGGCCGCGCTCT  
CTGTCACCCCTGGGCCTCTTTGCAGTGGAGCTGGCCGGTTTCCTCTCAGGAGTCTCCATGTTCAAC  
AGCACCCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGTGGCCCTGTCCTTCTTCAT  
ATTGAGCGTTGGGAGTGCACTACGTATTGGTACATTTTTGTCTTCTGCAGTGGCCTTCCAGCTG  
TCACTGAAATGGCTTTATTCGTCACCGTCTTTGGGCTGAAAAGAAACCCTTCTGATTACCTTCA  
TGACGGGAACCTAAGGACGAAGCCTACAGGGGCAAGGGCCGCTTCGTATTCTGGAAGAAGGAAG  
GCATAGGCTTCGGTTTTTCCCTCGGAAACTGCTTCTGCTGGAGGATATGTGTTGGAATAATTACG  
TCTTGAGTCTGGGATTATCCGCATTGTATTTAGTGCTTTGTAATAAAATATGTTTTGTAGTAACA  
TTAAGACTTATATACAGTTTtaggggacaattaaaaaaaaaaaa

## **FIGURE 90**

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLGLFA  
VELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCALPAVTEMALFV  
TVFGLKKKPF

**Transmembrane domain:**

amino acids 12-28 (type II), 51-66, 107-124

## FIGURE 91

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAGATGCAACTGAC  
TCGCTGCTGCTTCGTGTTCTTGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGGATGATG  
GTCCTCCCGGCTCAGAGGACCCTGAGCGTGATGACCACGAGGGCCAGCCCCGGCCCCGGGTGCCT  
CGGAAGCGGGGCCACATCTCACCTAAGTCCCGCCCCATGGCCAATTCCACTCTCCTAGGGCTGCT  
GGCCCCGCCTGGGGAGGCTTGGGGCATTCTTGGGCAGCCCCCAACCGCCCGAACCACAGCCCCC  
CACCTCAGCCAAGGTGAAGAAAATCTTTGGCTGGGGCGACTTCTACTCCAACATCAAGACGGTG  
GCCCTGAACCTGCTCGTCACAGGAAGATTGTGGACCATGGCAATGGGACCTTCAGCGTCCACTT  
CCAACACAATGCCACAGGCCAGGGAACATCTCCATCAGCCTCGTGCCCCCAGTAAAGCTGTAG  
AGTTCCACCAGGAACAGCAGATCTTCATCGAAGCCAAGGCCTCCAAAATCTTCAACTGCCGGATG  
GAGTGGGAGAAGGTAGAACGGGGCCGCGGACCTCGCTTTCACCCACGACCCAGCCAAGATCTG  
CTCCCGAGACCACGCTCAGAGCTCAGCCACCTGGAGCTGCTCCCAGCCCTTCAAAGTCGTCTGTG  
TCTACATCGCCTTCTACAGCACGGACTATCGGCTGGTCCAGAAGGTGTGCCCAGATTACAACATAC  
CATAGTGATACCCCTTACTACCCATCTGGGTGACCCGGGGCAGGCCACAGAGGCCAGGCCAGGGC  
TGGAAGGACAGGCCTGCCCATGCAGGAGACCATCTGGACACCGGGCAGGGAAGGGGTGGGCCTC  
AGGCAGGGAGGGGGGTGGAGACGAGGAGATGCCAAGTGGGGCCAGGGCCAAGTCTCAAGTGGCAG  
AGAAAGGGTCCCAAGTGCTGGTCCCAACCTGAAGCTGTGGAGTGACTAGATCACAGGAGCACTGG  
AGGAGGAGTGGGCTCTCTGTGCAGCCTCACAGGGCTTTGCCACGGAGCCACAGAGAGATGCTGGG  
TCCCCGAGGCCTGTGGGCAGGCCGATCAGTGTGGCCCCAGATCAAGTCATGGGAGGAAGCTAAGC  
CCTTGGTTCTTGCCATCCTGAGGAAAGATAGCAACAGGGAGGGGGAGATTTTCATCAGTGTGGACA  
GCCTGTCAACTTAGGATGGATGGCTGAGAGGGCTTCTTAGGAGCCAGTCAGCAGGGTGGGGTGGG  
GCCAGAGGAGCTCTCCAGCCCTGCCTAGTGGGCGCCCTGAGCCCCTTGTCTGTGTGCTGAGCATGG  
CATGAGGCTGAAGTGGAACCCTGGGGTCTTTGATGTCTTGACAGATTGACCATCTGTCTCCAGC  
CAGGCCACCCCTTTCCAAAATTCCTCTTCTGCCAGTACTCCCCCTGTACCACCCATTGCTGATG  
GCACACCCATCCTTAAGCTAAGACAGGACGATTGTGGTCTCCACACTAAGGCCACAGCCCATC  
CGCGTGCTGTGTGTCCCTCTTCCACCCCAACCCCTGCTGGCTCCTCTGGGAGCATCCATGTCCCG  
GAGAGGGGTCCCTCAACAGTCAGCCTCACCTGTCAGACGGGGTCTCCCGGATCTGGATGGCGC  
CGCCCTCTCAGCAGCGGGCACGGGTGGGGCGGGGCCGGCCGAGAGCATGTGCTGGATCTGTTC  
TGTGTGTCTGTCTGTGGGTGGGGGAGGGGAGGAAGTCTTGTGAAACCGTGATTGCTGACTTT  
TGTGTGAAGAATCGTGTCTTGGAGCAGGAAATAAAGCTTGCCCCGGGGCA

## **FIGURE 92**

MQLTRCCFVFLVQGSLLYLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMANSTL  
LGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVDHGNGTF  
SVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMWEKVERGRRTSLCTHDP  
AKICSRDHAQSSATWSCSQPFKVVVCVYIAFYSTDYRLVQKVC PDYNYHSDTPYYPSG

**Important features of the protein:**

**Signal peptide:**

amino acids 1-14

**N-glycosylation sites.**

amino acids 62-65, 127-130, 137-140, 143-146

**2-oxo acid dehydrogenases acyltransferase**

amino acids 61-71

## FIGURE 93

CGGTGGCCATGACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCTTCGGGCCTGCGCTCGCC  
CTTTATGTCTTCACCATCGCCATCGAGCCGTTGCGTATCATCTTCCTCATCGCCGGAGCTTCTT  
CTGGTTGGTGTCTCTACTGATTTTCGTCCCTTGTTTGGTTCATGGCAAGAGTCATTATTGACAACA  
AAGATGGACCAACACAGAAATATCTGCTGATCTTTGGAGCGTTTGTCTCTGTCTATATCCAAGAA  
ATGTTCCGATTTGCATATTATAAACTCTTAAAAAAGCCAGTGAAGGTTTGAAGAGTATAAACCC  
AGGTGAGACAGCACCCCTCTATGCGACTGCTGGCCTATGTTTCTGGCTTGGGCTTGGGAATCATGA  
GTGGAGTATTTTCCTTTGTGAATACCCTATCTGACTCCTTGGGGCCAGGCACAGTGGGCATTTCAT  
GGAGATTCTCCTCAATTCTTCCTTTATTCAGCTTTCATGACGCTGGTCATTATCTTGCTGCATGT  
ATTCTGGGGCATTGTATTTTTTGATGGCTGTGAGAAGAAAAAGTGGGGCATCCTCCTTATCGTTC  
TCCTGACCCACCTGCTGGTGTGTCAGCCCAGACCTTCATAAGTTCTTATTATGGAATAAACCTGGCG  
TCAGCATTTATAATCCTGGTGTCTATGGGCACCTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCG  
AAGCCTGAAACTCTGCCTGCTCTGCCAAGACAAGAAGCTTCTTCTTTACAACCAGCGCTCCAGAT  
AACCTCAGGGAACCAGCACTTCCCAAACCGCAGACTACATCTTTAGAGGAAGCACAACTGTGCCT  
TTTTCTGAAAATCCCTTTTTCTGGTGGAATTGAGAAAGAAATAAACTATGCAGATA

## **FIGURE 94**

MTAAVFFGCAFIAFGPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDNKDG  
PTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGFGIMSGV  
FSFVNTLSDSLGP GTVGIHGDS PQFFLYSAFMTLVIILLHVFWGIVFFDGCEKKKWGILLIVLLT  
HLLVSAQTFISSYYGINLASAFIILVIMGTWAF LAAGGSCRS LKCLLCQDKNFLLYNQRSR

**Important features of the protein:**

**Signal peptide:**

amino acids 1-19

**Transmembrane domains:**

amino acids 32-51, 119-138, 152-169, 216-235

**Glycosaminoglycan attachment site.**

amino acids 120-123

**Sodium:neurotransmitter symporter family protein**

amino acids 31-65

## FIGURE 95

AATTTTTACCAGAGTAACTTGAGAAACCAACTGGACCTTGAGTATTGTACATTTTGCCTCGTG  
GACCCAAAGGTAGCAATCTGAAACATGAGGAGTACGATTCTACTGTTTTGTCTTCTAGGATCAAC  
TCGGTCATTACCACAGCTCAAACCTGCTTTGGGACTCCCTCCCACAAACTGGCTCCGGATCAGG  
GAACACTACCAAACCAACAGCAGTCAAATCAGGTCTTTCCTTCTTTAAGTCTGATACCATTAAAC  
CAGATGCTCACACTGGGGCCAGATCTGCATCTGTTAAATCCTGCTGCAGGAATGACACCTGGTAC  
CCAGACCCACCCATTGACCTGGGAGGGTTGAATGTACAACAGCAACTGCACCCACATGTGTTAC  
CAATTTTTGTCACACAACCTGGAGCCCAGGGCACTATCCTAAGCTCAGAGGAATTGCCACAAATC  
TTCACGAGCCTCATCATCCATTCTTGTTCCTGGGAGGCATCCTGCCACCAGTCAGGCAGGGGC  
TAATCCAGATGTCCAGGATGGAAGCCTTCCAGCAGGAGGAGCAGGTGTAATCCTGCCACCCAGG  
GAACCCAGCAGGCCGCCTCCCAACTCCCAGTGGCACAGATGACGACTTTGCAGTGACCACCCCT  
GCAGGCATCCAAAGGAGCACACATGCCATCGAGGAAGCCACCACAGAATCAGCAAATGGAATTCA  
GTAAGCTGTTTCAAATTTTTTCAACTAAGCTGCCTCGAATTTGGTGATACATGTGAATCTTTATC  
ATTGATTATATTATGGAATAGATTGAGACACATTGGATAGTCTTAGAAGAAATTAATTCTTAATT  
TACCTGAAAATATTCTTGAAATTCAGAAAATATGTTCTATGTAGAGAATCCCAACTTTTAAAAA  
CAATAATTCATGGATAAATCTGTCTTTGAAATATAACATTATGCTGCCTGGATGATATGCATAT  
TAAACATATTTGAAAACCTGGAAA  
AAA

## **FIGURE 96**

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSLSLIPLTQM  
LTLGPDHLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPIFVTQLGAQGTILSSEE  
LPQIFTSLIIHSLFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGTPAGRLPTPSG  
TDDDFAVTTPAGIQRSTHAIEEATTESANGIQ

**Signal peptide:**

amino acids 1-16



[illegible][illegible]

## **FIGURE 98**

MVPAWLWLLCVSPQALPKAQAELSVEVPENYGGNFPLYLTKLPLPREGAEGQIVLSGDSGKAT  
EGPFAMDPDSGFLLVTRALDREEQAEYQLQVTLEMQDGHVLWGPQPVLVHVKDENDQVPHFSQAI  
YRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQSPDMFQLEPRLGALALSPKG  
STSLDHALERTYQLLVQVKMDQASGHQATATVEVSI IESTWVSLEPIHLAENLKVLYPHHMAQ  
VHWSGGDVHYHLESHPPGPFVNAEGNLYVTRELDREAQAEYLLQVRAQNSHGEDIAAPLELHVL  
VMDENDNVPICPPRDPTVSIPELSPPGTEVTRLAEDADAPGSPNSHVYQLLSPEPEDGVEGRA  
FQVDPTSGSVTLGVLPLRAGQNILLVLAMDLAGAEGGFSSTCEVEVAVTDINDHAPEFITSQIG  
PISLPEDVEPGTLVAMLTADADLEPAFRLMDFAIERGDTEGTFGLDWEPDSGHVRLRLCKNLSY  
EAAPSHEVVVVVQSVAKLVGPGPGGATATVTVLVERVMPPPKLDQESYEASVPI SAPAGSFLLT  
IQPSDPISRTLRFSLVNDSEGWLCIEKFSGEVHTAQSLQGAQPGDTYTVLVEAQDTALT LAPVPS  
QYLCTPRQDHGLIVSGPSKDPDLASGHGPYSFTLGPNPTVQRDWRLQTLNGSHAYLTALHWVEP  
REHIIPVVVSHNAQMWQLLVRVIVCRCNVEGQCMRKVGRMKGMPTKLSAVGILVGTTLVAIGIFLI  
LIFTHWTMSRKKDPDQPADSVPLKATV

### **Signal peptide:**

amino acids 1-18

### **Transmembrane domain:**

amino acids 762-784

## FIGURE 99

GGCTGACCGTGCTACATTGCCTGGAGGAAGCCTAAGGAACCCAGGCATCCAGCTGCCCACGCCTG  
AGTCCAAGATTCTTCCCAGGAACACAAACGTAGGAGACCCACGCTCCTGGAAGCACCAGCCTTTA  
TCTCTTACCTTCAAGTCCCCTTTCTCAAGAATCCTCTGTTCTTTGCCCTCTAAAGTCTTGGTAC  
ATCTAGGACCCAGGCATCTTGCTTTCCAGCCACAAAGAGACAGATGAAGATGCAGAAAGGAAATG  
TTCTCCTTATGTTTGGTCTACTATTGCATTTAGAAGCTGCAACAAATCCAATGAGACTAGCACC  
TCTGCCAACTGGATCCAGTGTGATCTCCAGTGGAGCCAGCACAGCCACCAACTCTGGGTCCAG  
TGTGACCTCCAGTGGGGTCAGCACAGCCACCATCTCAGGGTCCAGCGTGACCTCCAATGGGGTCA  
GCATAGTCACCAACTCTGAGTTCATACAACCTCCAGTGGGATCAGCACAGCCACCAACTCTGAG  
TTCAGCACAGCGTCCAGTGGGATCAGCATAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGG  
GGCCAGCACAGCCACCAACTCTGAGTCCAGCACACCCTCCAGTGGGGCCAGCACAGTCAACCACT  
CTGGGTCCAGTGTGACCTCCAGTGGAGCCAGCACTGCCACCAACTCTGAGTCCAGCACAGTGTCC  
AGTAGGGCCAGCACTGCCACCAACTCTGAGTCTAGCACACTCTCCAGTGGGGCCAGCACAGCCAC  
CAACTCTGACTCCAGCACAACTCCAGTGGGGCTAGCACAGCCACCAACTCTGAGTCCAGCACAA  
CCTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACT  
GCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAG  
AACGACCTCCAATGGGGCTGGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGGGGCCA  
GCACAGCCACCAACTCTGACTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAG  
TCCAGCACGACCTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGG  
GGCTAGCACAGCCACCAACTCTGACTCCAGCACAACTCCAGTGGGGCCGGCACAGCCACCAACT  
CTGAGTCCAGCACAGTGTCCAGTGGGATCAGCACAGTCAACCAATTCTGAGTCCAGCACACCCTCC  
AGTGGGGCCAAACAGCCACCAACTCTGAGTCCAGTACGACCTCCAGTGGGGCCAAACAGCCAC  
CAACTCTGAGTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAGCACAA  
CCTCCAGTGGGGTCAGCACAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCTAGCACA  
GCCACCAACTCTGACTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCTAG  
CACAGTGTCCAGTGGGATCAGCACAGTCAACCAATTCTGAGTCCAGCACAACTCCAGTGGGGCCA  
ACACAGCCACCAACTCTGGGTCCAGTGTGACCTCTGCAGGCTCTGGAACAGCAGCTCTGACTGGA  
ATGCACACAACCTCCCATAGTGATCTACTGCAGTGTGAGGCAAAGCCTGGTGGGTCCCTGGT  
GCCGTGGGAAATCTTCTCATCACCTGGTCTCGGTTGTGGCGGCCGTGGGGCTCTTTGCTGGGC  
TCTTCTTCTGTGTGAGAAACAGCCTGTCCCTGAGAAACACCTTTAACACAGCTGTCTACCACCCT  
CATGGCCTCAACCATGGCCTTGGTCCAGGCCCTGGAGGGAATCATGGAGCCCCCAGGCCCCAG  
GTGGAGTCCTAACTGGTTCTGGAGGAGACCAGTATCATCGATAGCCATGGAGATGAGCGGGAGGA  
ACAGCGGGCCCCTGAGCAGCCCCGGAAGCAAGTGCCGCATTCTTCAGGAAGGAAGAGACCTGGGCA  
CCCCAGACCTGGTTTCTTTTATTCATCCCAGGAGACCCCTCCAGCTTTGTTTGAATCCTGAA  
AATCTGAAGAAGGTATTCTTCTACCTTTCTTGCCTTTACCAGACACTGGAAAGAGAATACTATAT  
TGCTCATTTAGCTAAGAAATAAATACATCTCATCTAACACACACGACAAAGAGAAGCTGTGCTTG  
CCCCGGGTGGGTATCTAGCTCTGAGATGAATCAGTTATAGGAGAAAACCTCCATGCTGGATC  
CATCTGCGATTCAAAATCTCCACAGTAAATCCAAAGACCTCAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 100**

MMQKGNVLLMFGLLLHLEAATNSNETSTSANTGSSVISSGASTATNSGSSVTSSGVSTATISGS  
SVTSNGVSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTTSSGASTATNSESSTPSS  
GASTVTNSGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSSTTSSGASTA  
TNSESSTTSSGASTATNSESSTVSSRASTATNSESSTTSSGASTATNSESRTTSNGAGTATNSES  
STTSSGASTATNSDSSTVSSGASTATNSESSTTSSGASTATNSESSTTSSGASTATNSDSSTTSS  
GAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGANTATNSESSTVSSGASTA  
TNSESSTTSSGVSTATNSESSTTSSGASTATNSDSSTTSSEASTATNSESSTVSSGISTVTNSES  
STTSSGANTATNSGSSVTSAGSGTAALTGMHTTSHSASTAVSEAKPGGSLVPWEIFLITLVSVVA  
AVGLFAGLFFCVRNLSLRNTFNTAVYHPHGLNHGLGPGPGNHGAPHRPRWSPNWFRRPVSSI  
AMEMSGRNSGP

### **Signal peptide:**

amino acids 1-20

### **Transmembrane domain:**

amino acids 510-532

## FIGURE 101

GGCCGGACGCCTCCGCGTTACGGGATGAATTAACGGCGGGTTCCGCACGGAGGTTGTGACCCCTA  
CGGAGCCCCAGCTTGCCACGCACCCCACTCGGCGTCGCGCGGCGTGCCCTGCTTGTCACAGGTG  
GGAGGCTGGAATATCAGGCTGAAAAACAGAGTGGGTACTCTCTTCTGGGAAGCTGGCAACAAAT  
GGATGATGTGATATATGCATTCCAGGGGAAGGGAATTTGTGGTGCTTCTGAACCCATGGTCAATT  
AACGAGGCAGTTTCTAGCTACTGCACGTACTTCATAAAGCAGGACTCTAAAAGCTTTGGAATCAT  
GGTGTCATGGAAAGGATTTACTTTTATACTGACTCTGTTTTGGGGAAGCTTTTTTGAAGCATT  
TCATGCTGAGTCCCTTTTTACCTTTGATGTTTGTAACCCATCTTGGTATCGCTGGATCAACAAC  
CGCCTTGTGGCAACATGGCTCACCTACCTGTGGCATTATTGGAGACCATGTTTGGTGTAAGT  
GATTATAACTGGGGATGCATTTGTTCTGGAGAAAGAGTGTCATTATCATGAACCATCGGACAA  
GAATGGACTGGATGTTTCTGTGGAATTGCTGTGATGCGATATAGCTACCTCAGATTGGAGAAAATT  
TGCCCTCAAAGCGAGTCTCAAAGGTGTTCTGGATTTGGTTGGGCCATGCAGGCTGCTGCCTATAT  
CTTCATTATAGGAAATGGAAGGATGACAAGAGCCATTTCGAAGACATGATTGATTACTTTTGTG  
ATATTCACGAACCACTTCAACTCCTCATATTTCCAGAAGGGACTGATCTCACAGAAAACAGCAAG  
TCTCGAAGTAATGCATTTGCTGAAAAAATGGACTTCAGAAATATGAATATGTTTTACATCCAAG  
AACTACAGGCTTTACTTTTGTGGTAGACCGTCTAAGAGAAGGTAAGAACCTTGATGCTGTCCATG  
ATATCACTGTGGCGTATCCTCACAACATTCTCAATCAGAGAAGCACCTCCTCCAAGGAGACTTT  
CCCAGGGAAATCCACTTTACCGTCCACCGGTATCCAATAGACACCTCCCCACATCCAAGGAGGA  
CCTTCAACTCTGGTGCCACAAACGGTGGGAAGAGAAAGAGAGGCTGCGTTCTTCTATCAAG  
GGGAGAAGAATTTTTATTTTACCGGACAGAGTGTCATTCCACCTTGCAAGTCTGAAGTCAAGGTC  
CTTGTGGTCAAATTGCTCTCTATACTGTATTGGACCTGTTTCAGCCCTGCAATGTGCCTACTCAT  
ATATTTGTACAGTCTTGTTAAGTGGTATTTTATAATCACCATTGTAATCTTTGTGCTGCAAGAGA  
GAATATTTGGTGGACTGGAGATCATAGAACTTGCAATGTTACCGACTTTTACACAAACAGCCACAT  
TTAAATTCAAAGAAAAATGAGTAAGATTATAAGGTTTGCCATGTGAAAACCTAGAGCATATTTTG  
GAAATGTTCTAAACCTTTCTAAGCTCAGATGCATTTTTCATGACTATGTGAATATTTCTTACT  
GCCATCATTATTTGTTAAAGATATTTGCACTTAATTTTGTGGGAAAAATATTGCTACAATTTTT  
TTTAATCTCTGAATGTAATTTGATACTGTGTACATAGCAGGGAGTGATCGGGGTGAAATAACTT  
GGGCCAGAATATTATTAAACAATCATCAGGCTTTTAAA

## **FIGURE 102**

MHSRGREIVLLNPWSINEAVSSYCTYFIKQDSKSGIMVSWKGIYFILTLFWGSFFGSI FMLSP  
FLPLMFVNPSWYRWINNRLVATWLTLPVALLETMFGVKVIITGDAFVPGERSVIIMNHRTRMDWM  
FLWNCLMRYSYLRLEKICLKASLKGVPFGFWAMQAAAYIFIHRKWKDDKSHFEDMIDYFCDIHEP  
LQLLI FPEGTDLTENSKSRNAFAEKNGLQKYEYVLHPRTTGFTFVVDRLREGKNLDAVHDITVA  
YPHNIPQSEKHL LQGDFPREIH FHVHRYPIDTLPTSKE DLQWCHKRWEEKEERLRSFYQGEKNF  
YFTGQSVIPPCKSELRLVVKLLSILYWTLFSPAMCLLIYLYSLVKWYFIITIVIFVLQERIFGG  
LEI IELACYRL LHKQPHLNSKKNE

**Important features of the protein:**

**Signal peptide:**

amino acids 1-22

**Transmembrane domains:**

amino acids 44-63, 90-108, 354-377

## FIGURE 103

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCCTGCGCCTGAGACAGCTGGCCTGACC  
TCCAAATCATCCATCCACCCCTGCTGTCATCTGTTTTCATAGTGTGAGATCAACCCACAGGAATA  
TCCATGGCTTTTGTGCTCATTGTTGTTCTCAGTTTCTACGAGCTGGTGTGAGGACAGTGGCAAGT  
CACTGGACCGGGCAAGTTTGTCCAGGCCTGGTGGGGGAGGACGCCGTGTTCTCCTGCTCCCTCT  
TTCTGAGACCACTGCAGAGGCTATGGAAGTGGGTTCTTCAGGAATCAGTTCCATGCTGTGGTC  
CACCTCTACAGAGATGGGAAGACTGGGAATCTAAGCAGATGCCACAGTATCGAGGGAGAAGTGA  
GTTTGTGAAGGACTCCATTGCAGGGGGGCGTGTCTCTAAGGCTAAAAACATCACTCCCTCGG  
ACATCGGCCTGTATGGGTGCTGGTTTCAGTTCACAGATTACGATGAGGAGGCCACCTGGGAGCTG  
CGGGTGGCAGCACTGGGCTCACTTCCTCTCATTTCCATCGTGGGATATGTTGACGGAGGTATCCA  
GTTACTCTGCCCTGCTCAGGCTGGTTCCCCAGCCACAGCCAAGTGGAAAGGTCACAAGGAC  
AGGATTTGTCTTCAGACTCCAGAGCAAATGCAGATGGGTACAGCCTGTATGATGTGAGATCTCC  
ATTATAGTCCAGGAAAATGCTGGGAGCATATTGTGTTCCATCCACCTTGCTGAGCAGAGTCATGA  
GGTGAATCCAAGGTATTGATAGGAGAGACGTTTTTCCAGCCCTCACCTTGGCGCCTGGCTTCTA  
TTTTACTCGGGTTACTCTGTGGTGCCCTGTGTGGTGTGTCATGGGGATGATAATTGTTTTCTTC  
AAATCCAAAGGAAAAATCCAGCGGAACTGGACTGGAGAAGAAAGCAGGACAGGCAGAATTGAG  
AGACGCCCCGAAACACGCAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCG  
TTTTCTGATCTGAAAAGTGAACCCATAGAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGA  
TTTACAAGGAAGAGTGTGGTGGCTTCTCAGGGTTTCCAAGCAGGGAGACATTACTGGGAGGTGGA  
CGTGGGACAAAATGTAGGGTGGTATGTGGGAGTGTGTCGGGATGACGTAGACAGGGGGAAGAACA  
ATGTGACTTTGTCTCCCAACAATGGGTATTGGGTCTCAGACTGACAACAGAACATTTGTATTTT  
ACATTCAATCCCCATTTTATCAGCCTCCCCCAGCACCCCTCCTACACGAGTAGGGGTCTTCCT  
GGACTATGAGGGTGGGACCATCTCCTTCTTCAATACAAATGACCAGTCCCTTATTTATACCCTGC  
TGACATGTCAGTTTGAAGGCTTGTGAGACCCTATATCCAGCATGCGATGTATGACGAGGAAAAG  
GGGACTCCCATATTCATATGTCCAGTGTCTGGGGATCAGACAGAGAAGACCTGCTTAAAGGGC  
CCCACACCACAGACCAGACACAGCCAAGGGAGAGTGTCTCCGACAGGTGGCCCCAGCTTCTCT  
CCGGAGCCTGCGCACAGAGAGTACGCCCCCCTCTCTTTAGGGAGCTGAGGTTCTTCTGCCC  
TGAGCCCTGCAGCAGCGGCAGTCCAGCTTCCAGATGAGGGGGGATTGGCCTGACCTGTGGGAG  
TCAGAAGCCATGGCTGCCCTGAAGTGGGGACGGAATAGACTCACATTAGGTTTAGTTTGTGAAAA  
CTCCATCCAGCTAAGCGATCTTGAACAAGTCACAACCTCCAGGCTCCTCATTTGCTAGTCACGG  
ACAGTGATTCTGCTCAGAGTGAAGATTAAAGAGACAACGAATGTGAATCATGCTTGAGGTT  
TGAGGGCACAGTGTGCTAATGATGTGTTTTTATATTATACATTTCCACCATAAACTCTGTT  
TGCTTATTCCACATTAATTTACTTTTCTCTATACCAAATCACCCATGGAATAGTTATTGAACACC  
TGCTTTGTGAGGCTCAAAGAATAAAGAGGAGGTAGGATTTTCACTGATTCTATAAGCCCAGCAT  
TACCTGATACCAAACCAGGCAAAGAAAACAGAAGAAGAGGAAGGAAAACCTACAGGTCCATATCC  
CTCATTAACACAGACACAAAAATTTCTAAATAAAATTTTAAACAAATTAACCTAAACAATATATTTA  
AAGATGATATATACTACTCAGTGTGGTTTTGTCCACAAATGCAGAGTTGGTTTAAATATTTAAAT  
ATCAACCAGTGTAATTCAGCACATTAATAAAGTAAAAAGAAAACATAAAAAAAAAAAAAA

## **FIGURE 104**

MAFVLILVLSFYELVSGQWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVREFRNQFHAVVH  
LYRDGEDWESKQMPQYRGRTEFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEEATWELR  
VAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPQGQDLSSDSRANADGYSLYDVEISI  
IVQENAGSILCSIHLAEQSHEVESKVLIGETFFQSPWRLASILLGLLCGALCGVVMGMIIVFFK  
SKGKIQAELDWRKKGQAELRDARKHAVEVTLDPETAHPKLCVSDLKTVTHRKAQEVPHSEKRF  
TRKSVVASQGFQAGRHYWEVDVGQNVGWYGVCRDDVDRGKNNVTLSPNNGYWVLRLTTEHLYFT  
FNPHFISLPPSTPPTRVGVFLDYEGGTISFFNTNDQSLIYTLLTCQFEGLLRPYIQHAMYDEEKG  
TPIFICPVSWG

### **Signal peptide:**

amino acids 1-17

### **Transmembrane domains:**

amino acids 131-150, 235-259



## FIGURE 105

CCTTCACAGGACTCTTCATTGCTGGTTGGCAATGATGTATCGGCCAGATGTGGTGAGGGCTAGGAAAAGAG  
TTTGTTGGGAACCCCTGGGTTATCGGCCTCGTCATCTTCATATCCCTGATTGTCTGGCAGTGTGCATTGGA  
CTCACTGTTTCATTATGTGAGATATAATCAAAGAAGACCTACAATTACTATAGCACATTGTCATTTACAAC  
TGACAAACTATATGCTGAGTTTGGCAGAGAGGCTTCTAACAATTTACAGAAATGAGCCAGAGACTTGAAT  
CAATGGTGAAAAATGCATTTTATAAATCTCCATTAAGGGAAGAATTTGTCAAGTCTCAGGTTATCAAGTTC  
AGTCAACAGAAGCATGGAGTGTGGCTCATATGCTGTTGATTTGTAGATTTCACTCTACTGAGGATCCTGA  
AACTGTAGATAAAATTTGTTCAACTTGTTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCCCTAAAGTAG  
ATCCTCACTCAGTTAAATTAATAAATCAACAAGACAGAAACAGACAGCTATCTAAACCATTGCTGCGGA  
ACACGAAGAAGTAAACTCTAGGTCAGAGTCTCAGGATCGTTGGTGGGACAGAAGTAGAAGAGGGTGAATG  
GCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGTGGAGCAACCTTAATTAATGCCACATGGC  
TTGTGAGTGTGCTCACTGTTTTACAACATATAAGAACCCTGCCAGATGGACTGCTTCCTTTGGAGTAACA  
ATAAAACCTTCGAAAATGAAACGGGGTCTCCGGAGAATAATTGTCCATGAAAAATACAAACCCCCATCACA  
TGACTATGATATTTCTCTGTCAGAGCTTTCTAGCCCTGTTCCTACACAAATGCAGTACATAGAGTTTGTCT  
TCCCTGATGCATCCTATGAGTTTCAACCAGGTGATGTGATGTTTGTGACAGGATTTGGAGCACTGAAAAAT  
GATGGTTACAGTCAAATCATCTTCGACAAGCACAGGTGACTCTCATAGACGCTACAACTTGCAATGAACC  
TCAAGCTTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCTTAGAAGGAAAAACAGATGCAT  
GCCAGGGTGACTCTGGAGGACCACTGGTTAGTTCAGATGCTAGAGATATCTGGTACCTTGCTGGAATAGTG  
AGCTGGGGAGATGAATGTGCGAAACCAACAAGCCTGGTGTATATACTAGAGTTACGGCCTTGCGGGACTG  
GATTACTTCAAAAACCTGGTATCTAAGAGACAAAAGCCTCATGGAACAGATAACATTTTTTTTTGTTTTTG  
GGTGTGGAGGCCATTTTTAGAGATACAGAATTGGAGAAGACTTGCAAACAGCTAGATTTGACTGATCTCA  
ATAAACTGTTTGCTTGATGCATGTATTTCTTCCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTGCCA  
GATCAACTCTGTCTCTGTGAGCAATAGTTGAACTTTATGTACATAGAGAAATAGATAATACAATATTAC  
ATTACAGCCTGTATTCATTTGTTCTCTAGAAGTTTGTGAGAATTTTGACTTGTGACATAAATTTGTAAT  
GCATATATACAATTTGAAGCACTCCTTTCTTCACTCAGTCTCCTCATTTCAGCAAATATCCATTT  
TCAAGGTGCAGAACAGGAGTGAAGAAAAATATAAGAAGAAAAAATCCCTACATTTTATTGGCACAGAA  
AAGTATTAGGTGTTTTCTTAGTGAATATTAGAAATGATCATATTCATTATGAAAGTCAAGCAAAGACA  
GCAGAATACCAATCACTTCATCATTTAGGAAGTATGGGAAGTAAGTTAAGGAAGTCCAGAAAGAAGCCAAG  
ATATATCCTTATTTTCATTTCCAAACAACACTACTATGATAAATGTGAAGAAGATTCTGTTTTTTGTGACCT  
ATAATAATTATACAACTTCATGCAATGTACTTGTCTAAGCAAATTAAGCAAATATTTATTTAACATTG  
TTACTGAGGATGTCAACATATAACAATAAATATAAATCACCCA

## **FIGURE 106**

MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTYNYYSTLSFTTDKLY  
AEFGREASNNFTEMSQRLESMVKNAFYKSPLREEFVKSQVIKFSQQKHGVLAHMLLICRFHSTED  
PETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTLGQSLRIVGG  
TEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFGVTIKPSKMKRGL  
RRIIVHEKYKHPSHDYDISLAELSSPVPTNAVHRVCLPDASYEFQPGDVMFVTGFGALKNDGYS  
QNHLRQAQVTLIDATTCNEPQAYNDAITPRMLCAGSLEGKTDACQGDSGGPLVSSDARDIWYLAG  
IVSWGDECAKPNKPGVYTRVTALRDWITSKTGI

**Transmembrane domain:**

amino acids 21-40 (type II)

## FIGURE 107

AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCCTG  
CCCCGATGAGCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCACCAGGGCCAGC  
GCCGACGATCGTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGATGGGGCTTCTCCCTT  
ACGGGGCTCACAAATGGGCCAGAGAAGATTCCGTGAAGTGTCTGCGCTGCCTGCTCTACGCCCTCAA  
TCTGCTCTTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTTTCTGCTTGGATGAGGGACTACCTAA  
ATAATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTCATTTTGACTTACTTTCT  
GTGGTTCATCCGGTCATGATTGCTGTTTGTGTTTCTTATCATTGTGGGGATGTTAGGATATTG  
TGGAACGGTGAAAGAAATCTGTTGCTTCTTGCATGGTACTTTGGAAGTTTGTGTTGCTATTTCT  
GTGTAGAACTGGCTTGTGGCGTTTGGACATATGAACAGGAACCTATGGTTCCAGTACAATGGTCA  
GATATGGTCACTTTGAAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCA  
TGCTTGGAAATTTTTTTCAGAGAGAGTTTAAAGTGTCTGTGGAGTAGTATATTTCACTGACTGGTTGG  
AAATGACAGAGATGGACTGGCCCCAGATTCTGCTGTGTAGAGAATCCCAGGATGTTCCAAA  
CAGGCCCCACCAGGAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAAGAAAATGTATTCCTT  
TTTGAGAGGAACCAACAACCTGAGGTGCTGAGGTTTCTGGAATCTCCATTGGGGTGACACAAA  
TCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGGAGCCTGGG  
ACAGACCAATGATGTCCTTGAAGAATGACAACTCTCAGCACCTGTCATGTCCCTCAGTAGAACT  
GTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCCATGGCAAACAGCTTTAATACACACT  
TTGAGATGGAGGAGTTATATAAAAAGAAATGTCACAGAAGAAAACCACAACTTGTTTTATTGGACT  
TGTGAATTTTTGAGTACATACTATGTGTTTCAGAAATATGTAGAAATAAAAATGTTGCCATAAAA  
TAACACCTAAGCATATACTATTCTATGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAAGTC  
ACCACCTGGACAATAATTGATGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCC  
TGTGTATGACTTTTACTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCGCGA  
TCCATGCAAACGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGTTGATTTACTTCTACCAA  
CTAGTATATAAAGTACTAATTAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTA  
CTCAGCGATCTATTCTTCTGATGCTAAATAAATATATATCAGAAAACTTTCAATATTGGTGACT  
ACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACTTAAAAGAGCAAGCTAACACAT  
TGTCCTAAGCTGATCAGGGATTTTTGTATATAAGTCTGTGTTAAATCTGTATAATTCAGTCGAT  
TTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAATTTGTCCTGTATAGCATCATT  
ATTTTTAGCCTTTCTGTTAATAAAGCTTTACTATTCTGTCCTGGGCTTATATTACACATATAAC  
TGTTATTTAAATACTTAACCACTAATTTTGAAAATTACCAGTGTGATACATAGGAATCATTTATTC  
AGAATGTAGTCTGGTCTTTAGGAAGTATTAATAAGAAAATTTGCACATAACTTAGTTGATTTCAGA  
AAGGACTTGTATGCTGTTTTCTCCCAAATGAAGACTCTTTTGACACTAAACACTTTTTAAAAA  
GCTTATCTTTGCCTTCTCAAACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAA  
TAGTGTCTTTTTCTCCAGAAAAATGCTTGTGAGAATCATTAACATGTGACAATTTAGAGATT  
CTTTGTTTTATTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAATTTTTTTACAA  
GAGTATAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGATTTTGTAT  
TTCTCAGAATATGGAAAGAAAATTAATGTGTCAATAAATATTTTCTAGAGAGTAA

## **FIGURE 108**

MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTTLTAETRVEEAVILTYFPVVHP  
VMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWVTEQELMVPVQWSDMVT  
LKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTMDWPPDSCCVREFPGCSKQAHQ  
EDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWALYYDRREP GTDQM  
MSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL

### **Signal peptide:**

amino acids 1-33

### **Transmembrane domains:**

amino acids 12-35, 57-86, 94-114, 226-248

## FIGURE 109

CCAAGGCCAGAGCTGTGGACACCTTATCCCACCTCATCCTCTTCTCTGATAAAGCCCCCTACCAGTGCT  
GATAAAGTCTTTCTCGTGAGAGCCTAGAGGCCCTAAAAAAGTGCTTGAAAGAGAAGGGGACAAAGGAACA  
CCAGTATTAAGAGGATTTTCCAGTGTTCCTGGCAGTTGGTCCAGAAGGATGCCTCCATTCTGCTTCTCACCTG  
CCTCTTCATCACAGGCACCTCCGTGTCAACCGTGGCCCTAGATCCTTGTCTGCTTACATCAGCCTGAATGAGC  
CCTGGAGGAACACTGACCACCACTTGGATGAGTCTCAAGGTCTCTCTATGTGACAACCATGTGAATGGGGAG  
TGGTACCACCTTCACGGGCATGGCGGGAGATGCCATGCCTACCTTCTGCATACCAGAAAACCACTGTGGAACCCA  
CGCACCTGTCTGGCTCAATGGCAGCCACCCCTAGAAGGCGACGGCATTGTGCAACGCCAGGCTTGTGCCAGCT  
TCAATGGGAACCTGCTGTCTCTGGAACACCACGGTGAAGTCAAGGCTTGCCCTGGAGGCTACTATGTGTATCGT  
CTGACCAAGCCCAGCGTCTGCTTCCACGTCTACTGTGGTCATTTTTATGACATCTGCGACGAGGACTGCCATGG  
CAGCTGCTCAGATACCAGCGAGTGCACATGCGCTCCAGGAAGTGTGCTAGGCCCTGACAGGCAGACATGCTTTG  
ATGAAAATGAATGTGAGCAAAACACGGTGGCTGCAGTGAGATCTGTGTGAACCTCAAAAACCTCTACCCTGT  
GAGTGTGGGGTTGGCGTGTGCTAAGAAGTGATGGCAAGACTTGTGAAGACGTTGAAGGATGCCACAATAACAA  
TGGTGGCTGCAGCCACTCTTGCCTTGGATCTGAGAAAGGCTACCAGTGTGAATGTCCCCGGGGCTGGTGTGT  
CTGAGGATAACCACACTTGCCAAGTCCCTGTGTTGTGCAAAATCAAATGCCATTGAAGTGAACATCCCCAGGGAG  
CTGGTTGGTGGCTGGAGCTCTTCTGACCAACACCTCTGCCGAGGAGTGTCCAACGGGACCCATGTCAACAT  
CCTCTTCTCTCTCAAGACATGTGGTACAGTGGTGCATGTGGTGAATGACAAGATTGTGGCCAGCAACCTCGTGA  
CAGGTCTACCCAAGCAGACCCCGGGGAGCAGCGGGGACTTCATCATCCGAACCAGCAAGCTGCTGATCCCGGTG  
ACCTGCGAGTTTCCACGCCTGTACACCATTTCTGAAGGATACGTTCCCAACCTTCGAAACTCCCCACTGGAAAT  
CATGAGCCGAAATCATGGGATCTTCCCATTCACCTCTGGAGATCTTCAAGGACAATGAGTTTGAAGAGCCTTACC  
GGGAAGCTCTGCCACCCCTCAAGCTTCGTGACTCCCTCTACTTTGGCATTGAGCCCGTGGTGCACGTGAGCGGC  
TTGGAAGCTTGGTGGAGAGCTGCTTTGCCACCCCACTCCAAGATCGACGAGGTCTGAAATACTACCTCAT  
CCGGGATGGCTGTGTTTCAGATGACTCGGTAAAGCAGTACACATCCCGGGATCACCTAGCAAAGCACTTCCAGG  
TCCCTGTCTTCAAGTTTGTGGGCAAGACCACAAGGAAGTGTTCGCACTGCCGGGTTCTTGTCTGTGGAGTG  
TTGACGAGCGTTCCCGCTGTGCCAGGGTTGCCACCGCGAATGCGTCGTGGGGCAGGAGGAGGACTCAGC  
CGGTCTACAGGGCCAGACGCTAACAGGCGGCCGATCCGCATCGACTGGGAGGACTAGTTCGTAGCCATACCTC  
GAGTCCCTGCATTGGACGGCTCTGCTCTTTGGAGCTTCTCCCCCACCGCCCTCTAAGAACATCTGCCAACAGC  
TGGGTTCCAGACTTCACACTGTGAGTTCAGACTCCAGCACCACTCACTCTGATTCTGGTCCATTAGTGGGCA  
CAGGTACAGCACTGCTGAACAATGTGGCCTGGGTGGGTTTCATCTTCTAGGGTTGAAAATAAACTGTCCA  
CCCAGAAAGACACTCACCCATTTCCCTCATTTCTTCTTACACTTAATAACCTCGTGTATGGTGAATCAGAC  
CACAAAATCAGAAGCTGGGTATAATATTTCAAGTTACAAACCCTAGAAAATTAACAGTTACTGAATTATGA  
CTTAAATACCCAATGACTCCTTAAATATGTAAATTATAGTTATACCTTGAAATTTCAATTCAAATGCAGACTAA  
TTATAGGGAATTTGGAAGTGTATCAATAAACAGTATATAATTTT

## **FIGURE 110**

MPPFLLLTCLFITGTSVSPVALDPCSAYISLNEPWRNTDHLDESQGPPLCDNHVNGEWYHFTGMAGDAMP  
TFCIPENHCGTHAPVWLNGSHPLEGDGIVQRQACASFNGNCCLWNTTVEVKACPGGYVYRLTKPSVCFHV  
YCGHFYDIDCEDCHGSCSDTSECTCAPGTVLGPDRQTCFDENECEQNNGGCSEICVNLKNSYRCECGVGRV  
LRSDGKTCEDEVEGCHNNNGGCSHSLGSEKGYQCECPRGLVLSNHTCQVPVLCKSNAIEVNIPRELVGG  
LELFLTNTSCRGVSNNGTHVNILFSLKTCGTVVDVNDKIVASNLVTGLPKQTPGSSGDFIIRTSKLLIPVT  
CEFPRLYTISEGYVPNLRNSPLEIMSRNHGIFPFTLEIFKDNEFEOPYREALPTLKLKRDLSLYFGIEPVVHV  
SGLESLVESCFATPTSKIDEVLKYYLIRDGCVSDDSVKQYTSRDHLAKHFQVPVFKFVGKDHKEVFLHCRV  
LVCVGLDERSRCAQGCHRMRRGAGGEDSAGLQGQTLTGGPPIRIDWED

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-16

#### **N-glycosylation sites.**

amino acids 89-93, 116-120, 259-263, 291-295, 299-303

#### **Tyrosine kinase phosphorylation sites.**

amino acids 411-418, 443-451

#### **N-myristoylation sites.**

amino acids 226-232, 233-239, 240-246, 252-258, 296-302, 300-306,  
522-528, 531-537

#### **Aspartic acid and asparagine hydroxylation site.**

amino acids 197-209

#### **ZP domain proteins.**

amino acids 431-457

#### **Calcium-binding EGF-like proteins.**

amino acids 191-212, 232-253

## FIGURE 111

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCTGCCCTGCACTCGG  
GCCTCCTCCAGCCAGTGTCTGACCAGGGACTTCTGACCTGCTGGCCAGCCAGGACCTGTGTGGGGAGGCCCT  
CCTGCTGCCTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAGACCGGGAGGATCACAGAGCCAGCATGT  
TACAGGATCCTGACAGTGATCAACCTCTGAACAGCCTCGATGTCAAACCCCTGCGCAAACCCCGTATCCCC  
ATGGAGACCTTCAGAAAGGTGGGGATCCCCATCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGT  
GGTTGTCTCATCAAGGTGATTCTGGATAAACTACTTCTCTGCGGGCAGCCTCTCCACTTCATCCCGA  
GGAAGCAGCTGTGTGACGGAGAGCTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTTC  
CCCGAAGGGCCTGCAGTGGCAGTCCGCCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGGACTCGGCCAC  
AGGGAACCTGGTTCTCTGCCTGTTTCGACAACCTTCACAGAAGCTCTCGCTGAGACAGCCTGTAGGCAGATGG  
GCTACAGCAGAGCTGTGGAGATTGGCCCCAGACCAGGATCTGGATGTTGTTGAAATCACAGAAAACAGCCAG  
GAGCTTCGCATGCGGAACCTCAAGTGGGCCCTGTCTCTCAGGCTCCCTGGTCTCCCTGCAGTGTCTTGCCTG  
TGGGAAGAGCCTGAAGACCCCCCGTGTGGTGGGTGGGGAGGAGGCTCTGTGGATTCTTGGCCTTGGCAGG  
TCAGCATCCAGTACGACAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCTCACGGCA  
GCCCCACTGCTTCAGGAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAAACTGGGCAG  
CTTCCCATCCCTGGCTGTGGCCAAGATCATCATCATTGAATTCAACCCCATGTACCCCAAAGACAATGACA  
TCGCCCTCATGAAGCTGCAGTTCCCACTCACTTTCTCAGGCACAGTCAGGCCCATCTGTCTGCCCTTCTTT  
GATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTGGATGGGGCTTTACGAAGCAGAATGGAGGGAA  
GATGTCTGACATACTGCTGCAGGCGTCAGTCCAGGTCATTGACAGCACACGGTGCAATGCAGACGATGCGT  
ACCAGGGGGAAGTCACCGAGAAGATGATGTGTGCAGGCATCCCGGAAGGGGGTGTGGACACCTGCCAGGGT  
GACAGTGGTGGGCCCCCTGATGTACCAATCTGACCAGTGGCATGTGGTGGGCATCGTTAGCTGGGGCTATGG  
CTGCGGGGGCCCCGAGCACCCCAAGGATATACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATGTCT  
GGAAGGCTGAGCTGTAATGCTGCTGCCCCCTTTCAGTGTCTGGGAGCCGCTTCCTTCTGCTGCCCTGCCACCT  
GGGGATCCCCCAAAGTCAGACACAGAGCAAGAGTCCCCCTGGGTACACCCCTCTGCCCACAGCCTCAGCAT  
TTCTTGGAGCAGCAAAGGGCCTCAATTCTGTAAAGAGCCCTCGCAGCCCAGAGGCGCCCAGAGGAAGTCA  
GCAGCCCTAGCTCGGCCACACTTGGTGTCTCCAGCATCCCGGGAGAGACACAGCCCACTGAACAAGGTCT  
CAGGGGTATTGCTAAGCCAAGAAGGAAC'TTCCCACACTACTGAATGGAAGCAGGCTGTCTTGTAAGGCC  
CAGATCACTGTGGCTGGAGAGGAGAAGGAAAGGTCTGCGCCAGCCCTGTCCGTCTTACCCATCCCCAA  
GCCTACTAGAGCAAGAAACCAGTTGTAATATAAAATGCACTGCCCTACTGTTGGTATGACTACCGTTACCT  
ACTGTTGTATTGTTATTACAGCTATGGCCACTATTATTAAAGAGCTGTGTAACATCTCTGGCAAAAAAAA  
AAAA

## **FIGURE 112**

MLQDPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIALLSLASIIIVVVLIKVILDKYYFLCG  
QPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWFSACFDN  
FTEALAETACRQMGYSRAVEIGPDQDLVDVEITENSQELMRNSSGPGCLSGSLVSLHCLACGKSL  
KTPRVVGEEASVDSWPWQVSIQYDKQHVCSSILDPHWLTAAHCFRKHTDVFNWKVRAGSDKL  
GSFPSLAVAKIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTPATPLWIIIGWG  
FTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTCCQGDSSGGLMYQS  
DQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL

**Transmembrane domain:**

amino acids 32-53 (typeII)



## FIGURE 113

GGCTGGACTGGAACCTCCTGGTCCCAAGTGATCCACCCGCTCAGCCTCCCAAGGTGCTGTGATTA  
TAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACCTTTTCAGCAACTAAAAAGCCACAGGAGT  
TGAAGTGTAGGATTCTGACTATGCTGTGGTGGCTAGTGCTCCTACTCCTACCTACATTAAAAATC  
TGTTTTTTGTTCTCTTGTAACTAGCCTTTACCTTCCTAACACAGAGGATCTGTCACTGTGGCTCT  
GGCCCAAACCTGACCTTCACTCTGGAACGAGAACAGAGGTTTCTACCCACACCGTCCCCTCGAAG  
CCGGGGACAGCCTCACCTTGTGGCCTCTCGCTGGAGCAGTGCCCTCACCAACTGTCTCACGTCT  
GGAGGCACTGACTCGGGCAGTGCAGGTAGCTGAGCCTCTTGGTAGCTGCGGCTTTCAAGGTGGGC  
CTTGCCCTGGCCGTAGAAGGGATTGACAAGCCCCGAAGATTTTCATAGGCGATGGCTCCCCTGCCC  
AGGCATCAGCCTTGTGTAGTCAATCACTGCCCTGGGGCCAGGACGGGCCGTGGACACCTGCTCA  
GAAGCAGTGGGTGAGACATCACGCTGCCCCGCCATCTAACCTTTTCATGTCCTGCACATCACCTG  
ATCCATGGGCTAATCTGAACTCTGTCCCAAGGAACCCAGAGCTTGAGTGAGCTGTGGCTCAGACC  
CAGAAGGGGTCTGCTTAGACCACCTGGTTTATGTGACAGGACTTGCAATTCTCCTGGAACATGAGG  
GAACGCCGGAGGAAAGCAAAGTGGCAGGGAAGGAACTTGTCGCAAAATATGGGTCAGAAAAGATG  
GAGGTGTTGGGTATCACAAAGGCATCGAGTCTCCTGCATTCAAGTGGACATGTGGGGGAAGGGCTG  
CCGATGGCGCATGACACACTCGGGACTCACCTCTGGGGCCATCAGACAGCCGTTTCCGCCCCGAT  
CCACGTACCAGCTGCTGAAGGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCAGCCAAAA  
TCTGCGATCACCAGCCAGGGGCAGCCGTCTGGGAAGGAGCAAGCAAAGTGACCATTTCTCCTCCC  
CTCCTTCCCTCTGAGAGGCCCTCCTATGTCCCTACTAAAGCCACCAGCAAGACATAGCTGACAGG  
GGCTAATGGCTCAGTGTTGGCCCAGGAGGTGAGCAAGGCTGAGAGCTGATCAGAAGGGCCTGCT  
GTGCGAACACGGAAATGCCTCCAGTAAGCACAGGCTGCAAAATCCCCAGGCAAAGGACTGTGTGG  
CTCAATTTAAATCATGTTCTAGTAATTGGAGCTGTCCCCAAGACCAAAGGAGCTAGAGCTTGTT  
CAAATGATCTCCAAGGGCCCTTATACCCAGGAGACTTTGATTTGAATTTGAAACCCCAAATCCA  
AACCTAAGAACCAGGTGCATTAGAATCAGTTATTGCCGGGTGTGGTGGCCTGTAATGCCAACAT  
TTTGGGAGGCCGAGGCGGTAGATCACCTGAGGTGAGGAGTTCAAGACCAGCCTGGCCAACATGG  
TGAAACCCCTGTCTCTACTAAAAATACAAAAAACTAGCCAGGCATGGTGGTGTGTGCTGTATC  
CCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGTGAAGGAGGCTGAGACA  
GGAGAATCACTTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGAAAAATAAAAAAGAATTA  
TGGTTATTTGTAA

## **FIGURE 114**

MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTASPC  
WPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRRD

Signal peptide:  
amino acids 1-15

## FIGURE 115

CAGCAGTGGTCTCTCAGTCCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACCATGGCAA  
AGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCCAAGAAA  
ATATGTAAATCACTTAAGATTTGTGGACTGGTGTGTTGGTATCCTGGCCCTAACTCTAATTGTCCT  
GTTTTGGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAGCCTATGACATGGAGCACACTT  
TCTACAGCAATGGAGAGAAGAAGAAGATTTACATGGAAATTGATCCTGTGACCAGAACTGAAATA  
TTCAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACTTTAAAAACGGATACACTGG  
CATCTACTTCGTGGGTCTTCAAAAATGTTTTATCAAACTCAGATTAAAGTGATTCCTGAATTTT  
CTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACCACAACCTTTCTTTGAACAGTCAGTG  
ATTTGGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGATTTTCTTAAAAATTCCAAAATTCTGGA  
GATTTGTGATAACGTGACCATGTATTGGATCAATCCCACTCTAATATCAGTTTCTGAGTTACAAG  
ACTTTGAGGAGGAGGGAGAAGATCTTCACTTTCCTGCCAACGAAAAAAGGGATTGAACAAAAT  
GAACAGTGGGTGGTCCCTCAAGTGAAAGTAGAGAAGACCCGTCACGCCAGACAAGCAAGTGAGGA  
AGAACTTCCAATAAATGACTATACTGAAAATGGAATAGAATTTGATCCCATGCTGGATGAGAGAG  
GTTATTGTTGTATTTACTGCCGTCGAGGCAACCGCTATTGCCGCCGCGTCTGTGAACCTTTACTA  
GGCTACTACCCATATCCATACTGCTACCAAGGAGGACGAGTCATCTGTCGTGTCATCATGCCTTG  
TAACTGGTGGGTGGCCCGCATGCTGGGGAGGGTCTTAATAGGAGGTTTGAGCTCAAATGCTTAAAC  
TGCTGGCAACATATAATAAATGCATGCTATTCAATGAATTTCTGCCTATGAGGCATCTGGCCCT  
GGTAGCCAGCTCTCCAGAATTACTTGTAGGTAATTCCTCTCTTCATGTTCTAATAAACTTCTACA  
TTATCACCAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 116**

MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPPKAYDME  
HTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLVHDFKNGYTGIFYVGLQKCFIKTQIKVIP  
EFSEPEEEIDENEEITTTFFEQSVIWPVPAEKPIENRDFLKNSKILEICDNVTMYWINPTLISVSE  
LQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDYTENGIEFDPMLD  
ERGYCCIIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVICRVIMPCNWWVARMMLGRV

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-40

#### **Transmembrane domain:**

amino acids 25-47 (type II)

#### **N-glycosylation sites.**

amino acids 94-97, 180-183

#### **Glycosaminoglycan attachment sites.**

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-  
242

#### **N-myristoylation sites.**

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

#### **Microbodies C-terminal targeting signal.**

amino acids 315-317

#### **Cytochrome c family heme-binding site signature.**

amino acids 9-14

## FIGURE 117

GAGCTCCCCCTCAGGAGCGCGTTAGCTTCACACCTTCGGCAGCAGGAGGGCGGCAGCTTCTCGCAGGCGGCA  
GGGCGGGCGGCCAGGATCATGTCCACCACCACATGCCAAGTGGTGGCGTTCCCTCCTGTCCATCCTGGGGCT  
GGCCGGCTGCATCGCGGCCACCGGGATGGACATGTGGAGCACCAGGACCTGTACGACAACCCCGTCACCT  
CCGTGTTCAGTACGAAGGGCTCTGGAGGAGCTGCGTGAGGCAGAGTTCAGGCTTCACCGAATGCAGGCCC  
TATTTACCATCCTGGGACTTCCAGCCATGCTGCAGGCAGTGCAGCCCTGATGATCGTAGGCATCGTCTCCT  
GGGTGCCATTGGCCTCCTGGTATCCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTG  
CCAAAGCCAACATGACACTGACCTCCGGGATCATGTTTATTGTCTCAGGTCTTTGTGCAATTGCTGGAGTG  
TCTGTGTTTGCCAACATGCTGGTGACTAAGTCTGGATGTCCACAGCTAACATGTACACCGGCATGGGTGG  
GATGTGTGCAGACTGTTTCCAGACCAGGTACACATTTGGTGCGGCTCTGTTTCGTGGGCTGGGTGCGTGGAGGCC  
TCACACTAATTGGGGGTGTGATGATGTGCATCGCCTGCCGGGGCTGGCACCAGAAGAAACCAACTACAAA  
GCCGTTTCTTATCATGCCTCAGGCCACAGTGTTCCTACAAGCCTGGAGGCTTCAAGGCCAGCACTGGCTT  
TGGGTCCAACACCAAAAACAAGAAGATATACGATGGAGGTGCCCGCACAGAGGACGAGGTACAATCTTATC  
CTTCCAAGCAGCACTATGTGTAATGTCTCTAAGACCTCTCAGCACGGCGGAAGAACTCCCGGAGAGCTCA  
CCCAAAAACAAGGAGATCCCCTAGATTTCTTCTTGCTTTTGACTCACAGCTGGAAGTTAGAAAAGCCT  
CGATTTTCTCTTTGGAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATTCCACCATAAAACA  
GCTGAGTTATTTATGAATTAGAGGCTATAGCTCACATTTTCAATCCTCTATTTCTTTTTTAAATATAACT  
TTCTACTCTGATGAGAGAATGTGGTTTTAATCTCTCTCTCACATTTTGATGATTTAGACAGACTCCCCCTC  
TTCTCCTAGTCAATAAACCATTGATGATCTATTTCCAGCTTATCCCCAAGAAAACCTTTGAAAGGAAA  
GAGTAGACCCAAAGATGTATTTTCTGCTGTTTGAAATTTGTCTCCCCACCCCAACTTGGCTAGTAATAA  
ACACTTACTGAAGAAGAAGCAATAAGAGAAAGATATTTGTAATCTCTCCAGCCCATGATCTCGGTTTTCTT  
ACACTGTGATCTTAAAAGTTACCAAACCAAGTCATTTTCAGTTTGAGGCAACCAACCTTTCTACTGCTG  
TTGACATCTTCTTATTACAGCAACACCATTCTAGGAGTTTCTGAGCTCTCCACTGGAGTCTCTTTCTGT  
CGCGGGTCAGAAATTGTCCCTAGATGAATGAGAAAATTATTTTTTTAATTAAAGTCTAAATATAGTTAA  
AATAAATAATGTTTTAGTAAAATGATACACTATCTCTGTGAAATAGCCTCACCCCTACATGTGGATAGAAG  
GAAATGAAAAAATAATTGCTTTGACATTGTCTATATGGTACTTTGTAAAGTCATGCTTAAGTACAAATTC  
ATGAAAAGCTCACACCTGTAATCCTAGCACTTTGGGAGGCTGAGGAGGAAGGATCACTTGAGCCCAGAAGT  
TCGAGACTAGCCTGGGCAACATGGAGAAGCCCTGTCTCTACAAAATACAGAGAGAAAAATCAGCCAGTCA  
TGGTGGCATACACCTGTAGTCCCAGCATTCGGGAGGCTGAGGTGGGAGGATCACTTGAGCCCAGGGAGGT  
TGGGGCTGCAGTGAGCCATGATCACACCACTGCACCTCCAGCCAGGTGACATAGCGAGATCCTGTCTAAAAA  
AATAAAAAATAAATAATGAACACAGCAAGTCTAGGAAGTAGGTTAAACTAATTCTTTAA

## **FIGURE 118**

MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLWRSCVRQSSSGFTECRP  
YFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIMFIVSGL  
CAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTLIGGVMMCIA  
CRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTEDEVQSYPSKHDY  
V

### **Signal peptide:**

amino acids 1-23

### **Transmembrane domains:**

amino acids 81-100, 121-141, 173-194

## FIGURE 119

GGAAAACTGTTCTTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTCCGGAGTCC  
AGCTGGCTAAAACTCATCCCAGAGGATAATGGCAACCCATGCCTTAGAAATCGCTGGGCTGTTTCTTG  
GTGGTGTGGAAATGGTGGGCACAGTGGCTGTCACTGTGCCTCAGTGGAGAGTGTGGCCTTCATT  
GAAAACAACATCGTGGTTTTTGAAGAACTTCTGGGAAGGACTGTGGATGAATTGCGTGAGGCAGGCTAA  
CATCAGGATGCAGTGC AAAATCTATGATTCCCTGCTGGCTCTTTCTCCGGACCTACAGGCAGCCAGAG  
GACTGATGTGTGCTGCTTCCGTGATGTCTTCTTGGCTTTCATGATGGCCATCCTTGGCATGAAATGC  
ACCAGGTGCACGGGGGACAATGAGAAGGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTTCAT  
CATCACGGGCATGGTGGTGTCTATCCCTGTGAGCTGGGTTGCCAATGCCATCATCAGAGATTTCTATA  
ACTCAATAGTGAATGTTGCCAAAAACGTGAGCTTGGAGAAGCTCTCTACTTAGGATGGACCACGGCA  
CTGGTGCTGATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTTTTGTTGCAACGAAAAGAGCAGTAGCTA  
CAGATACTCGATACCTTCCCATCGCACAACCCAAAAAGTTATCACACCGGAAAGAAGTCACCGAGCG  
TCTACTCCAGAAGTCAGTATGTGTAGTTGTGTATGTTTTTTAACTTTACTATAAAGCCATGCAAATG  
ACAAAAATCTATATTACTTTCTCAAAATGGACCCCAAGAACTTTGATTTACTGTTCTTAACTGCCT  
AATCTTAATTACAGGAAGTGTGCATCAGCTATTTATGATTCTATAAGCTATTTACGCAGAATGAGATA  
TTAAACCCCAATGCTTTGATTGTTCTAGAAAGTATAGTAATTTGTTTTCTAAGGTGGTTCAAGCATCTA  
CTCTTTTTATCATTACTTCAAAATGACATTGCTAAAGACTGCATTATTTTACTACTGTAATTTCTCC  
ACGACATAGCATTATGTACATAGATGAGTGTAAACATTTATATCTCACATAGAGACATGCTTATATGGT  
TTTATTTAAAAATGAAATGCCAGTCCATTACACTGAATAAATAGAACTCAACTATTGCTTTTCAGGGAA  
ATCATGGATAGGGTTGAAGAAGGTTACTATTAATTGTTTAAAAACAGCTTAGGGATTAATGTCTCCCA  
TTTATAATGAAGATTAAATGAAGGCTTTAATCAGCATTGTAAAGGAAATTGAATGGCTTTCTGATAT  
GCTGTTTTTTAGCCTAGGAGTTAGAAATCCTAACTTCTTTATCCTCTTCTCCAGAGGCTTTTTTTTT  
CTTGTGTATTAAATTAACATTTTTAAAACGCAGATATTTGTCAAGGGGCTTTCATTCAAAGTCTT  
TTCCAGGGCTATACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATGGTTTTAGGAAAGTG  
AAAATATTTTTGTTTTGTTTTGAAGAAGATGATGCATTTTGACAAGAAATCATATATGTATGGAT  
ATATTTTAATAAGTATTTGAGTACAGACTTTGAGGTTTCATCAATATAAATAAAGAGCAGAAAAATA  
TGCTTGTTTTTCATTGCTTACCAAAAAACAACAACAAAAAAGTTGTCCTTTGAGAACTTCACCT  
GCTCCTATGTGGGTACCTGAGTCAAAATTGTCATTTTTGTTCTGTGAAAAATAAATTCCTTCTTGTA  
CCATTTCTGTTTAGTTTTACTAAATCTGTAAATACTGTATTTTTCTGTTTATTCCAAATTTGATGAA  
ACTGACAATCCAATTTGAAAGTTTGTGTCGACGTCTGTCTAGCTTAAATGAATGTGTCTATTGCTT  
TATACATTTATATTAATAAATTGTACATTTTTCTAATT

## **FIGURE 120**

MATHALEIAGLFLGGVGMVGTVAVTVMPPQWRVSAFIENNIVVFENFW EGLWMNCVRQANIRMQCK  
IYDSL LALSPDLQAARGLMCAASVMSFLAFMAILGMKCTRCTGDNEKVKAHILLTAGIIFIITG  
MVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLI VGGALFCCVFCCNEKSSSY  
RYSIPSHRTTQKSYHTGKKSPSVYSRSQYV

### **Signal peptide:**

amino acids 1-17

### **Transmembrane domains:**

amino acids 82-101, 118-145, 164-188



## FIGURE 121

GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGCGGAG  
CCAGACGCTGACCACGTTCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCGGCAGCC  
GGGAGCCATGCGACCCAGGGCCCCGCGCCTCCCCGAGCGGCTCCGCGGCCTCCTGCTGCTCC  
TGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAGCAAAGGCGCAG  
CTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGGGCCAGCAGGAGTGCC  
TGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTACACCTGGGATCCCAGGTGGGATG  
GATTCAAAGGAGAAAAGGGGAATGTCTGAGGGAAAGCTTTGAGGAGTCTGGACACCCAACTAC  
AAGCAGTGTTTCATGGAGTTCATTGAATTATGGCATAGATCTTGGGAAAATTGCGGAGTGATATT  
TACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTGTTCAGTGGCTCACTTCGGCTAAAATGCA  
GAAATGCATGCTGTCTAGCGTTGGTATTTTACATTCAATGGAGCTGAATGTTTCAAGACCTCTTCCC  
ATTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCG  
CACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGTCTGGATTAGTGGATGTTGCTATCTGGG  
TTGGCACTTGTTTCAAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATC  
ATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTTTTATTATGCC  
TTGGAATGGTTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAG  
CTAAATATGTTTACAGACCAAAGTGATTTTCACTGTTTTTAAATCTAGCATTATTCATTTTG  
CTTCAATCAAAGTGGTTTCAATATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATT  
CTCTCAACCTATAATTTGGAATATTGTTGTGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTTA  
AAAAAATATAAAGCTACCAATCTTTGTACAATTGTAAATGTTAAGAATTTTTTTTATATCTGT  
TAAATAAAAATTATTTCCAACA

## **FIGURE 122**

MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAAGVPGR  
DGSPGANVIPGTPGIPGRDGFKEGEGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIAECTFTK  
MRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIYLDQGSPEMNSTINIHRYS  
SVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEELPK

### **Signal peptide:**

amino acids 1-30

### **Transmembrane domain:**

amino acids 195-217

## FIGURE 123

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCTTCTGGGCTCCAACGCAGCTCTGTGGCTGAA  
 CTGGGTGCTCATCACGGGAAGTCTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAGCCCCAA  
 ATTGCCTGGAAGAATACATCATGTTTTTCGATAAGAAGAAATTGTAGGATCCAGTTTTTTTTTTA  
 ACCGCCCCCTCCCCACCCCCAAAAAACTGTAAAGATGCAAAAACGTAATATCCATGAAGATCC  
 TATTACCTAGGAAGATTTTGATGTTTTGCTGCGAATGCGGTGTGGGATTTATTTGTTCTTGGAG  
 TGTTCTGCGTGGCTGGCAAAGAATAATGTTCCAAAATCGGTCCATCTCCCAAGGGGTCCAATTTT  
 TCTTCCTGGGTGTCAGCGAGCCCTGACTCACTACAGTGCAGCTGACAGGGGCTGTGATGCAACTG  
 GCCCCAAGCCAAAGCAAAGACCTAAGGACGACCTTTGAACAATACAAAGGATGGGTTTCAATG  
 TAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTTATAGCCCCACTGTCTTACTGACAATG  
 CTTTCTTCTGCCGAACGAGGATGCCCTAAGGGCTGTAGGTGTGAAGGCAAAATGGTATATTGTGA  
 ATCTCAGAAATTACAGGAGATACCCTCAAGTATATCTGCTGGTTGCTTAGGTTTGTCCCTTCGCT  
 ATAACAGCCTTCAAAAACCTTAAGTATAATCAATTTAAAGGGCTCAACCAGCTCACCTGGCTATAC  
 CTTGACCATAACCATATCAGCAATATTGACGAAAATGCTTTTAAATGGAATACGCAGACTCAAAGA  
 GCTGATTCTTAGTTCCAATAGAAATCTCCTATTTTCTTAACAATACCTTCAGACCTGTGACAAATT  
 TACGGAACCTTGGATCTGTCTTATAATCAGCTGCATTCTCTGGGATCTGAACAGTTTCGGGGCTTG  
 CGGAAGCTGCTGAGTTTACATTTACGGTCTAACTCCCTGAGAACCATCCCTGTGCGAATATTCCA  
 AGACTGCCGCAACCTGGAACCTTTTGGACCTGGGATATAACCGGATCCGAAGTTTAGCCAGGAATG  
 TCTTTGCTGGCATGATCAGACTCAAAGAACCTTCACCTGGAGCACAATCAATTTTCCAAGCTCAAC  
 CTGGCCCTTTTCCAAGGTTGGTCAGCCTTCAGAACCTTTACTTGCAGTGGAAATAAATCAGTGT  
 CATAGGACAGACCATGTCTGGACCTGGAGCTCCTTACAAAGGCTTGATTTATCAGGCAATGAGA  
 TCGAAGCTTTTCAAGTGGACCCAGTGTTTTCCAGTGTGTCCCGAATCTGCAGCGCCTCAACCTGGAT  
 TCCAACAAGCTCACATTTATTGGTCAAGAGATTTTGGATTCTTGGATATCCCTCAATGACATCAG  
 TCTTGCTGGGAATATATGGAATGCAGCAGAAATATTGCTCCCTTGTAAGTGGCTGAAAAGTT  
 TTAAGGTCTAAGGGAGAATACAATTATCTGTGCCAGTCCCAAAGAGCTGCAAGGAGTAAATGTG  
 ATCGATGCAGTGAAGAATACAGCATCTGTGGCAAAAGTACTACAGAGAGGTTTGATCTGGCCAG  
 GGCTCTCCCAAAGCCGACGTTTAAAGCCCAAGCTCCCCAGGCCGAAGCATGAGAGCAAACCCCTT  
 TGCCCCGACGGTGGGAGCCACAGAGCCCGGCCAGAGACCGATGCTGACGCCGAGCACATCTCT  
 TTCCATAAAATCATCGCGGGCAGCGTGGCGCTTTTCTGTCCGTGCTCGTCATCTGCTGGTTAT  
 CTACGTGTGATGGAAGCGGTACCTGCGAGCATGAAGCAGCTGCAGCAGCGCTCCCTCATGCGAA  
 GGCACAGGAAAAAGAAAAGACAGTCCCTAAAGCAAATGACTCCAGCACCAGGAATTTATGTA  
 GATTATAAACCCACCAACACGGAGACCAGCGAGATGCTGCTGAATGGGACGGGACCTGCACCTA  
 TAACAAATCGGGTCCAGGGAGTGTGAGGTATGAACCATTGTGATAAAAAGAGCTCTTAAAAGCT  
 GGGAAATAAGTGGTCTTTATTGAACTCTGGTGACTATCAAGGGAACGCGATGCCCCCTCCCC  
 TTCCCTCTCCCTCTCACTTTGGTGGAAGATCCTTCCTTGTCCGTTTTAGTGCATTTCATAATACT  
 GGTCAATTTCTCTCATACATAATCAACCCATTGAAATTTAAATACCACAATCAATGTGAAGCTT  
 GAACTCCGGTTTAAATATAATACCTATTGTATAAGACCCCTTACTGATTCATTAAATGTGCGATT  
 GTTTTAAGATAAACTTCTTTCATAGGTAAAAA

## **FIGURE 124**

MGFNVIRLLSGSAVALVIAPTVELLTMSSAERGCPKGCRCEGKMVYCESQKLQEIPSSISAGCLG  
LSLRYNLSQKLKYNQFKGLNQLTWLYLDHNNHISNIDENAFNGIRRLKELILSSNRISYFLNNTFR  
PVTNLRNLDLSYNQLHSLGSEQFRGLRKLSSLHLRSNSLRITPVRIQDCRNLELLDLGYNRIRS  
LARNVFAGMIRLKEHLEHNQFSKLNALFPRLVSLQNLQWNKISVIGQTMSTWSSLRDL  
SGNEIEAFSGPSVFQCVNLQRLNLDNKLTFIQEILDSWISLNDISLAGNIWECSRNICSLVN  
WLKSFKGLRENTIICASPKELQGVNVIDAVKNYSICGKSTTERFDLARALPKPTFKPKLPRPKHE  
SKPPLPPTVGATEPGPETDADAEHISFHKIIAGSVALFLSVLVILLVIYVSWKRYPASMKQLQQR  
SLMRRHRKKRQSLKQMPSTQEFYVDYKPTNTETSEMLLNGTGPCTYNKSGSRECEV

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-33

#### **Transmembrane domain:**

amino acids 420-442

#### **N-glycosylation sites.**

amino acids 126-129, 357-360, 496-499, 504-507

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 465-468

#### **Tyrosine kinase phosphorylation site.**

amino acids 136-142

#### **N-myristoylation sites.**

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

## FIGURE 125

CCGTTATCGTCTTGCGCTACTGCTGAATGTCGTCGTCGCGGAGGAGGAGAGAGGCTTTTGCCGCTG  
ACCCAGAGATGGCCCCGAGCGAGCAAATTCCTACTGTCCGGCTGCGCGGCTACCGTGGCCGAGCT  
AGCAACCTTTCCCCTGGATCTCACAAAACTCGACTCCAAATGCAAGGAGAAGCAGCTCTTGCTC  
GGTTGGGAGACGGTGCAAGAGAATCTGCCCCCTATAGGGGAATGGTGCGCACAGCCCTAGGGATC  
ATTGAAGAGGAAGGCTTTCTAAAGCTTTGGCAAGGAGTGACACCCGCCATTTACAGACACGTAGT  
GTATTCTGGAGGTGCAATGGTCACATATGAACATCTCCGAGAGGTTGTGTTTGGCAAAAGTGAAG  
ATGAGCATTATCCCCTTTGGAAATCAGTCATTGGAGGGATGATGGCTGGTGTATTGGCCAGTTT  
TTAGCCAATCCAACCTGACCTAGTGAAGGTTTCAGATGCAAATGGAAGGAAAAAGGAACTGGAAGG  
AAAACCATTGCGATTTTCGTGGTGTACATCATGCATTTGCAAAAATCTTAGCTGAAGGAGGAATAC  
GAGGGCTTTGGGCAGGCTGGGTACCCAATATACAAAGAGCAGCACTGGTGAATATGGGAGATTTA  
ACCACTTATGATACAGTGAAACACTACTTGGTATTGAATACACCACTTGAGGACAATATCATGAC  
TCACGGTTTATCAAGTTTATGTTCTGGACTGGTAGCTTCTATTCTGGGAACACCAGCCGATGTCA  
TCAAAAGCAGAATAATGAATCAACCACGAGATAAACAAGGAAGGGGACTTTTGTATAAATCATCG  
ACTGACTGCTTGATTGAGGCTGTTCAAGGTGAAGGATTCATGAGTCTATATAAAGGCTTTTACC  
ATCTTGGCTGAGAATGACCCCTTGGTCAATGGTGTCTGGCTTACTTATGAAAAATCAGAGAGA  
TGAGTGGAGTCAGTCCATTTTAA

## **FIGURE 126**

MSVPEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMGEAALARLGDGARES  
APYRGMVRTALGIIEEGFLKLWQGVTPAIYRHVVYSGGRMVTYEHLREVVFVKSEDEHYPLWKS  
VIGGMMAGVIGQFLANPTDLVKVQMMEGKRKLEGKPLRFRGVHHAFAKILAEGGIRGLWAGWVP  
NIQRAALVNMGDLTTYDTVKHYLVNTPLEDNIMTHGLSSLCSGLVASILGTPADVIKSRIMNQP  
RDKQGRGLLYKSSTDCLIQAVQGEGFMSLYKGFLPSWLRMTPWSMVFWLTYEKIREMSGVSPF

**Transmembrane domains:**

amino acids 25-38, 130-147, 233-248

## FIGURE 127

CGCGGATCGGACCCAAGCAGGTCGGCGGGCGGCGGCAGGAGAGCGGCCGGGCGTCAGCTCCTCGAC  
CCCCGTGTCGGGCTAGTCCAGCGAGGCGGACGGGCGGCGTGGGCCCATGGCCAGGCCCGGCATGG  
AGCGGTGGCGCGACCGGCTGGCGCTGGTGACGGGGGCGCTCGGGGGGCATCGGCGCGGCCGTGGCC  
CGGGCCCTGGTCCAGCAGGGACTGAAGGTGGTGGGCTGCGCCCGCACTGTGGGCAACATCGAGGA  
GCTGGCTGCTGAATGTAAGAGTGCAGGCTACCCCGGGACTTTGATCCCCACAGATGTGACCTAT  
CAAATGAAGAGGACATCCTCTCCATGTTCTCAGCTATCCGTTCTCAGCACAGCGGTGTAGACATC  
TGCATCAACAATGCTGGCTTGGCCCGGCCTGACACCCTGCTCTCAGGCAGCACCAGTGGTTGGAA  
GGACATGTTCAATGTGAACGTGCTGGCCCTCAGCATCTGCACACGGGAAGCCTACCAGTCCATGA  
AGGAGCGGAATGTGGACGATGGGCACATCATTAACATCAATAGCATGTCTGGCCACCGAGTGTGA  
CCCCTGTCTGTGACCCACTTCTATAGTGCCACCAAGTATGCCGTCAGTGCCTGACAGAGGGACT  
GAGGCAAGAGCTTCGGGAGGCCCAGACCCACATCCGAGCCACGTGCATCTCTCCAGGTGTGGTGG  
AGACACAATTGCGCTTCAAACCTCCACGACAAGGACCCTGAGAAGGCAGCTGCCACCTATGAGCAA  
ATGAAGTGTCTCAAACCCGAGGATGTGGCCGAGGCTGTTATCTACGTCCTCAGCACCCCCGCACA  
CATCCAGATTGGAGACATCCAGATGAGGCCCACGGAGCAGGTGACCTAGTGACTGTGGGAGCTCC  
TCCTTCCCTCCCCACCCTTCATGGCTTGCCTCCTGCCTCTGGATTTTAGGTGTTGATTTCTGGAT  
CACGGGATACCATTCTGTCCACACCCCGACCAGGGGCTAGAAAATTTGTTTGAGATTTTATA  
TCATCTTGTCAAATTGCTTCAGTTGTAAATGTGAAAAATGGGCTGGGGAAAGGAGGTGGTGTCCC  
TAATTGTTTTACTTGTTAACTTGTCTTGTGCCCTGGGCACTTGGCCTTTGTCTGCTCTCAGTG  
TCTTCCCTTTGACATGGGAAAGGAGTTGTGGCCAAAATCCCCATCTTCTTGACCTCAACGTCTG  
TGGCTCAGGGCTGGGGTGGCAGAGGGAGGCCTTACCTTATATCTGTGTTGTTATCCAGGGCTCC  
AGACTTCCTCCTCTGCCTGCCCCACTGCACCCTCTCCCCCTTATCTATCTCCTTCTCGGCTCCCC  
AGCCCAGTCTTGGCTTCTTGTCCCCTCCTGGGGTCATCCCTCCACTCTGACTCTGACTATGGCAG  
CAGAACACCAGGGCCTGGCCCAGTGGATTTCATGGTGATCATTAAAAAGAAAAATCGCAACCAA  
AAAAAAAAAA

## **FIGURE 128**

MARPGMERWRDRLALVTGASGGIGAARALVQQGLKVVGCAITVGNIEELAAECKSAGYPGTLI  
PYRCDLSNEEDILSMFSAIRSQHSQVDICINNAGLARPDTLTSGSTSGWKDMFNVNVLALSICTR  
EAYQSMKERNVDDGHIININMSGHRVLPVSVTHFYATKYAVTALTEGLRQELREAQTHIRATC  
ISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVLSTPAHIQIGDIQMRPTEQVT

**Important features of the protein:**

**Signal peptide:**

amino acids 1-17

**N-myristoylation sites.**

amino acids 18-24, 21-27, 22-28, 24-30, 40-46, 90-96, 109-115,  
199-205

**Short-chain alcohol dehydrogenase.**

amino acids 30-42, 104-114



## FIGURE 129

AACTTCTACATGGGCCTCCTGCTGCTGGTGTCTTCTCAGCCTCCTGCCGGTGGCCTACACCAT  
CATGTCCCTCCCACCCTCCTTTGACTGCGGGCCGTTAGGTGCAGAGTCTCAGTTGCCCCGGAGC  
ACCTCCCCTCCCAGGCAGTCTGCTCAGAGGGCCTCGGCCAGAAATCCAGTTCTGGTTTCATGC  
CAGCCTGTAAAGGCCATGGAACTTTGGGTGAATCACCGATGCCATTTAAGAGGGTTTTCTGCCA  
GGATGGAAATGTTAGGTCGTTCTGTGTCTGCGCTGTTCAATTCAGTAGCCACCAGCCACCTGTGG  
CCGTTGAGTGCTTGAATGAGGAAGTGAAGAAATTAATTTCTCATGTATTTTCTCATTATTTA  
TTAATTTTAACTGATAGTTGTACATATTTGGGGGTACATGTGATATTTGGATACATGTATACAA  
TATATAATGATCAAAATCAGGGTAAGTGGGATATCCATCACATCAAACATTTATTTTTTATTCTTT  
TTAGACAGAGTCTCACTCTGTACCCAGGCTGGAGTGCAGTGGTGCCATCTCAGCTTACTGCAAC  
CTCTGCCTGCCAGGTTCAAGCGATTCTCATGCCTCCACCTCCCAAGTAGCTGGGACTACAGGCAT  
GCACCACAATGCCCAACTAATTTTTGTATTTTAGTAGAGACGGGGTTTTGCCATGTTGCCCAGG  
CTGGCCTTGAACCTCCTGGCCTCAAACAATCCACTTGCCTCGGCCTCCCAAAGTGTTATGATTACA  
GGCGTGAGCCACCGTGCCTGGCCTAAACATTTATCTTTTCTTGTGTGGGAACTTTGAAATTAT  
ACAATGAATTATTGTTAACTGTCACTCTCCCTGCTGTGCTATGGAACACTGGGACTTCTTCCCTCT  
ATCTAACTGTATATTTGTACCAGTTAACCAACCGTACTTCATCCCCACTCCTCTCTATCCTTCCC  
AACCTCTGATCACCTCATTCTACTCTCTACCTCCATGAGATCCACTTTTTTAGCTCCACATGTG  
AGTAAGAAAATGCAATATTTGTCTTTCTGTGCCTGGCTTATTTCACTTAACATAATGACTTCCTG  
TTCCATCCATGTTGCTGCAATGACAGGATTCGTTCTTAATTTCAATTAAATAACCACACATG  
GCAAAAA

## **FIGURE 130**

MGLLLLVLFLSLLPVAYTIMSLPPSFDCGPFRRCRVSVAREHLPSRGSLLRGPRPRIPVLVSCQPV  
KGHGTLGESPMPPFKRVFCQDGNVRSFCVCAVHFSSHQPPVAVECLK

Important features of the protein:

Signal peptide:

amino acids 1-18

N-myristoylation site.

amino acids 86-92

Zinc carboxypeptidases, zinc-binding region 2 signature.

amino acids 68-79

## FIGURE 131

TTCTGAAGTAACGGAAGCTACCTTGATATAAAGACCTCAACACTGCTGACCATGATCAGCGCAGCCTGGAGC  
ATCTTCCTCATCGGGACTAAAATTGGGCTGTTCTTCAAGTAGCACCTCTATCAGTTATGGCTAAATCCTG  
TCCATCTGTGTGCTGCGATGCGGGTTTCATTTACTGTAATGATCGCTTTCTGACATCCATTCCAACAG  
GAATACCAGAGGATGCTACAACCTCTTACCTTCAGAACAACCAAATAAATAATGCTGGGATTCTTCAGAT  
TTGAAAACTTGCTGAAAGTAGAAAGATATACCTATACCACAACAGTTTAGATGAATTTCTACCAACCT  
CCCAAAGTATGTAAAAGAGTTACATTTGCAAGAAAATAACATAAGGACTATCACTTATGATTCACTTTCAA  
AAATTCCTATCTGGAAGAATTACATTTAGATGACAACCTCTGTCTCTGCAGTTAGCATAGAAGAGGGAGCA  
TTCCGAGACAGCAACTATCTCCGACTGCTTTTCTGTCCCGTAATCACCTTAGCACAAATCCCTGGGGTTT  
GCCCAGGACTATAGAAGAACTACGCTTGGATGATAATCGCATATCCACTATTTTCATCACCATCTCTTCAAG  
GTCTCACTAGTCTAAAACGCCTGGTTCTAGATGGAACCTGTTGAACAATCATGGTTTAGGTGACAAAGTT  
TTCTTCAACCTAGTTAATTTGACAGAGCTGTCCCTGGTGCGGAATTCCTGACTGCTGCACCAAGTAAACCT  
TCCAGGCACAAACCTGAGGAAGCTTTATCTTCAAGATAACCAATCAATCGGGTGCCCCAAATGCTTTTT  
CTTATCTAAGGCAGCTCTATCGACTGGATATGTCCAATAATAACCTAAGTAATTTACCTCAGGGTATCTTT  
GATGATTTGGACAATATAACACAACCTGATTCTTCGCAACAATCCCTGGTATTGCGGGTGCAAGATGAAATG  
GGTACGTGACTGGTTACAATCACTACCTGTGAAGGTCAACGTGCGTGGGCTCATGTGCCAAGCCCCAGAAA  
AGGTTCTGGTGGGATGGCTATTAAGGATCTCAATGCAGAACTGTTTGATTGTAAGGACAGTGGGATTGTAAGC  
ACCATTGAGATAACCACTGCAATACCCAACACAGTGTATCCTGCCCAAGGACAGTGGCCAGCTCCAGTGAC  
CAAACAGCCAGATATTAAGAACCCCAAGCTCACTAAGGATCAACAAACCACAGGGAGTCCCTCAAGAAAA  
CAATTACAATTACTGTGAAGTCTGTACCTCTGATACCATTTCATATCTCTTGGAACCTTGCTCTACCTATG  
ACTGCTTTGAGACTCAGCTGGCTTAAACTGGGCCATAGCCCGGCATTGGATCTATAACAGAAACAATTGT  
AACAGGGGAACGCAGTGAGTACTTGGTCACAGCCCTGGAGCCTGATTCACCTATAAAGTATGCATGGTTT  
CCATGGAACACAGCAACCTCTACCTATTTGATGAACTCCTGTTTGTATTGAGACTGAACTGCACCCCTT  
CGAATGTACAACCTACAACCACCTCAATCGAGAGCAAGAGAAAGAACCTTACAAAAACCCAATTTACC  
TTTGGCTGCCATCATTGGTGGGGCTGTGGCCCTGGTTACCATTGCCCTTCTTGCTTTAGTGTGTTGGTATG  
TTCATAGGAATGGATCGCTCTTCTCAAGGAAGTGTGCATATAGCAAAGGGAGGAGAAGAAAGGATGACTAT  
GCAGAAGCTGGCACTAAGAAGGACAACCTCTATCCTGGAATCAGGGAACTTCTTTTCAGATGTTACCAAT  
AAGCAATGAACCCATCTCGAAGGAGGAGTTGTAATACACACCATATTTCTCCTAATGGAATGAATCTGT  
ACAAAAACAATCAGGTGAAGCAGTAGTAACCGAAGCTACAGAGACAGTGGTATTCCAGACTCAGATCAC  
TCACACTCATGATGCTGAAGGACTCACAGCAGACTTGTGTTTTGGGTTTTTTAAACCTAAGGGAGGTGATG  
GT

## **FIGURE 132**

MISAAWSIFLIGTKIGLFQVAPLSVMAKSCPSVCRCDAGFIYCNDRLTSIPTGIPEDATTLYL  
QNNQINNAGIPSDLKNLLKVERIYLYHNSLDEFPTNLPKYVKELHLQENNIRTITYDSLSKIPYL  
EELHLDNSVSAVSIEEGAFRDSNYLRLLFLSRNLSTIPWGLPRTIEELRLDDNRISTISSPSL  
QGLTSLKRLVLDGNLLNNHGLGDKVFFNLVNLTELSLVRNSLTAAPVNLPGTNLRKLYLQDNHIN  
RVPPNAFSYLRLQLYRLDMSNNLSNLPQGIFDDLDNITQLILRNNPWYCGCKMKWVRDWLQSLPV  
KVNVRGLMCQAPEKVRGMAIKDLNAELFDCKDSGIVSTIQITTAIPNTVYPAQGQWPAPVTKQPD  
IKNPKLTKDQQTGSPSRKTITITVKSVTSDTIHISWKLALPMTALRLSWLKLGHSPAFGSITET  
IVTGERSEYLVTALEPDSYKVCMPVEMETSNLYLFEDETPVCIETETAPLRMYNPPTTLNREQEKE  
PYKNPNPLAAIIGGAVALVTIALALVCWYVHRNGSLFSRNCAYSKGRRRKDDYAEAGTKKDNS  
ILEIRETSFQMLPISNEPISKEEFVIHTIFPPNGMNLKNNHSESSSNRSYRDSGIPDSHSHS

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-28

#### **Transmembrane domain:**

amino acids 531-552

#### **N-glycosylation sites.**

amino acids 226-229, 282-285, 296-299, 555-558, 626-629, 633-636

#### **Tyrosine kinase phosphorylation site.**

amino acids 515-522

#### **N-myristoylation sites.**

amino acids 12-17, 172-177, 208-213, 359-364, 534-539, 556-561,  
640-645

#### **Amidation site.**

amino acids 567-570

#### **Leucine zipper pattern.**

amino acids 159-180

#### **Phospholipase A2 aspartic acid active site.**

amino acids 34-44

## FIGURE 133

CCGTCATCCCCCTGCAGCCACCCTTCCCAGAGTCCTTTGCCAGGCCACCCAGGCTTCTTGGCA  
GCCCTGCCGGGCCACTTGTCTTCAATGTCTGCCAGGGGAGGTGGGAAGGAGGTGGGAGGAGGGCG  
TGCAGAGGCAGTCTGGGCTTGGCCAGAGCTCAGGGTGCTGAGCGTGTGACCAGCAGTGAGCAGAG  
GCCGGCCATGGCCAGCCTGGGGCTGCTGCTCCTGCTCTTACTGACAGCACTGCCACCGCTGTGGT  
CCTCCTCACTGCCTGGGCTGGACACTGCTGAAAGTAAAGCCACCATTGCAGACCTGATCCTGTCT  
GCGCTGGAGAGAGCCACCGTCTTCCTAGAACAGAGGCTGCCTGAAATCAACCTGGATGGCATGGT  
GGGGTCCGAGTGTGGAAGAGCAGCTAAAAAGTGTCCGGGAGAAGTGGGCCCAGGAGCCCCTGC  
TGCAGCCGCTGAGCCTGCGCGTGGGGATGCTGGGGGAGAAGCTGGAGGCTGCCATCCAGAGATCC  
CTCCACTACCTCAAGCTGAGTGATCCCAAGTACCTAAGAGAGTTCCAGCTGACCCCTCCAGCCGG  
GTTTTGGAAGCTCCACATGCCTGGATCCACACTGATGCCTCCTTGGTGTACCCACGTTCCGGGC  
CCCAGGACTCATTCTCAGAGGAGAGAAGTGACGTGTGCCTGGTGCAGCTGCTGGGAACCGGGACG  
GACAGCAGCGAGCCCTGCGGCCTCTCAGACCTCTGCAGGAGCCTCATGACCAAGCCCGGCTGCTC  
AGGCTACTGCCTGTCCCACCAACTGCTCTTCTCTCTGCGCCAGAATGAGGGGATGCACACAGG  
GACCACTCCAACAGAGCCAGGACTATATCAACCTCTTCTGCGCCAACATGATGGACTTGAACCGC  
AGAGCTGAGGGCCATCGGATACGCCCTACCCTACCCGGGACATCTTCATGGAAAACATCATGTTCTG  
TGGAATGGGCGGCTTCTCCGACTTCTACAAGCTCCGGTGGCTGGAGGCCATTCTCAGCTGGCAGA  
AACAGCAGGAAGGATGCTTCGGGGAGCCTGATGCTGAAGATGAAGAATTATCTAAAGCTATTCAA  
TATCAGCAGCATTTTTTCGAGGAGAGTGAAGAGGCGAGAAAAACAATTTCCAGATTCTCGCTCTGT  
TGCTCAGGCTGGAGTACAGTGGCGCAATCTCGGCTCACTGCAACCTTTGGCTCCTGGGTTCAAGC  
AATTCTCTTGCTCATCTCTCCGAGTAGCTGGGACTACAGGAGCGTGCCACCATACTGGCTAAT  
TTTTATATTTTTTTAGTAGAGACAGGGTTTTCATCATGTTGCTCATGCTGGTCTCGAACTCCTGAT  
CTCAAGAGATCCGCCACCTCAGGCTCCCAAAGTGTGGGATTATAGGTGTGAGCCACCGTGTCTG  
GCTGAAAAGCACTTTCAAAGAGACTGTGTTGAATAAAGGGCCAAGGTTCTTGCCACCCAGCACTC  
ATGGGGGCTCTCTCCCTAGATGGCTGCTCTCCCAACACAGCCACAGCAGTGGCAGCCCTGG  
GTGGCTTCCTATACATCCTGGCAGAATAACCCCCAGCAAACAGAGGCCACACCCATCCACACCG  
CCACCACCAAGCAGCCGCTGAGACGGACGGTTCCATGCCAGCTGCCTGGAGGAGGAACAGACCCC  
TTTAGTCCTCATCCCTTAGATCCTGGAGGGCACGGATCACATCCTGGGAAGAAGGCATCTGGAGG  
ATAAGCAAAGCCACCCCGACACCCAATCTTGGAAGCCCTGAGTAGGCAGGGCCAGGGTAGGTGGG  
GGCCGGGAGGGACCCAGGTGTGAACGGATGAATAAAGTTCAACTGCAACTGAAAAAAAAA

## **FIGURE 134**

MSARGRWEGGRRACRGSISGLARAQGAERTVSSEQRPAMASLGLLLLLLLTALPPLWSSSLPGLD  
TAESKATIADLILSALERATVFLEQRLPEINLDGMVGVRVLEEQLKSVREKWAQEPLLQPLSLRV  
GMLGEKLEAAIQRSLSHYLKLSDPKYLREFQLTLQPGFWKLPHAWIHTDASLVYPTFGPQDSFSEE  
RSDVCLVQLLGTGTDSSEPCGLSDLCRSLMTKPGCSGYCLSHQLLFFLWARMRGCTQGPLQQSQD  
YINLFCANMMDLNRRAEAIGYAYPTRDIFMENIMFCGMGGFSDFYKLRWLEAILSQKQEGCGFG  
EPDAEDEELSKAIQYQQHFSRRVKRREKQFPDSRSVAQAGVQWRNLGSLQPLPPGFKQFSCILIP  
SSWDYRSVPPYLANFYIFLVETGFHHVAHAGLELLISRPPTSGSQSVGL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 39-56

**Tyrosine kinase phosphorylation sites.**

amino acids 149-156, 274-282

**N-myristoylation sites.**

amino acids 10-16, 20-26, 63-69, 208-214

**Amidation site.**

amino acids 10-14

**Glycoprotein hormones beta chain signature 1.**

amino acids 230-237

## FIGURE 135

GGTCTGAGTGCAGAGCTGCTGTCATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTG  
CTGCTGCTATCGGGGATGTCCAGAGCTCGGAGGTGCCCCGGGGCTGCTGCTGAGGGATCGGGAGG  
GAGTGGGGTCGGCATAGGAGATCGCTTCAAGATTGAGGGCGTGCAGTTGTTCCAGGGGTGAAGC  
CTCAGGACTGGATCTCGGCGGCCCGAGTGTGGTAGACGGAGAAGAGCACGTCGGTTTCCCTTAAG  
ACAGATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGAAGTTGTATCTCC  
AGCTTACAGATTTGATCCCGTTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCAAGATATG  
TGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATGAAATCTTCAGGT  
CCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTTCTAATGAACCCAATGGT  
TATGATGATGGTTCTTCTTTATTGATATTTGTGCTTCTGCCTAAAGTGGTCAACACAAGTGATC  
CTGACATGAGACGGGAAATGGAGCAGTCAATGAATATGCTGAATTCCAACCATGAGTTGCCTGAT  
GTTTCTGAGTTCATGACAAGACTCTTCTCTTCAAAATCATCTGGCAAATCTAGCAGCGGCAGCAG  
TAAACAGGCAAAAGTGGGGCTGGCAAAGGAGGTAGTCAGGCCGTCCAGAGCTGGCATTTCAC  
AAACACGGCAACACTGGGTGGCATCCAAGTCTTGAAAACCGTGTGAAGCAACTACTATAAACTT  
GAGTCATCCCGACGTTGATCTCTTACAACGTGTATGTT  
AACTTTTGTAGCACATGTTTTGTACTTGGTACACGAGAAAACCCAGCTTTCATCTTTTGTCTGTAT  
GAGGTCAATATTGATGTCAGTGAATTAATTACAGTGTCCATAGAAAATGCCATTAATAAATTAT  
ATGAACTACTATACATTATGTATATTAATTAACATCTTAATCCAGAAATCAAAAAAAAAAAAA  
AAAAAAAAAAAAAA

## **FIGURE 136**

MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEKSGSGVGIGDRFKIEGRAVVPGVKPDWISAA  
RVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSAPYRFDVPRVDITSKGKMRARYVNYIKTSE  
VVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMVLPLLI FVLLPKVVNTSDPDMRREME  
QSMNMLNSNHELDPDVSEFMTRLFSSKSSGKSSSGSKTGKSGAGKRR

### **Important features of the protein:**

#### **Signal sequence:**

amino acids 1-23

#### **Transmembrane domain:**

amino acids 161-182

#### **N-glycosylation site.**

amino acids 184-187

#### **Glycosaminoglycan attachment sites.**

amino acids 37-40, 236-239

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 151-154

#### **N-myristoylation sites.**

amino acids 33-38, 36-41, 38-44, 229-234

#### **Amidation site.**

amino acids 238-241

#### **ATP/GTP-binding site motif A (P-loop).**

amino acids 229-236



## FIGURE 137

GATGGCGCAGCCACAGCTTCTGTGAGATTTCGATTTCTCCCCAGTTCCCCTGTGGGTCTGAGGGGA  
CCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATTCCCCAAAACAA  
GTTTTGACATTTCCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCTGTTCCAGGC  
CTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGCCACGACCTGTGC  
CACCAACTCGCACTCAGACTCTGAACTCAGACCTGAAATCTTCTCTTCACGGGAGGCTTGGCAGT  
TTTTCTTACTCCTGTGGTCTCCAGATTTCAGGCCTAAGATGAAAGCCTCTAGTCTTGCCCTCAGC  
CTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGGACTGAAGACACTCAATTTGGG  
AAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCTGAGATACGGGGCAGTG  
TGCAAGCCAAAGATGGAACATTGACATCAGAATCTTAAGGAGGACTGAGTCTTGCAAGACACA  
AAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTTGCTAAGACTCTATCTGGACAGGGTATTTAA  
AACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTCGCCAATTCCTTTCTTA  
CCATCAAGAAGGACCTCCGGCTCTCTCATGCCACATGACATGCCATTGTGGGGAGGAAGCAATG  
AAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGC  
TTTGGGGGAACTAGACATTCTTCTGCAATGGATGGAGGAGACAGAATAGGAGGAAAGTGATGCTG  
CTGCTAAGAATATTCGAGGTCAAGAGCTCCAGTCTTCAATACCTGCAGAGGAGGCATGACCCCAA  
ACCACCATCTCTTTACTGTACTAGTCTTGTGCTGGTCACAGTGTATCTTATTTATGCATTACTTG  
CTTCCTTGCAATGATTGTCTTTATGCATCCCCAATCTTAATTGAGACCATACTTGTATAAGATTTT  
TGTAATATCTTTCTGCTATTGGATATATTTATTAGTTAATATATTTATTTATTTTTTGCATTTTA  
ATGTATTTATTTTTTTACTTGGACATGAACTTTAAAAAAATTCACAGATTATATTTATAACCTG  
ACTAGAGCAGGTGATGTATTTTTATACAGTAAAAAAAACCTTGTAATTCAGAAAGAGTGG  
CTAGGGGGGTATTTCATTTGTATTCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGAT  
ATTTGAAATTGAACCAATGACTACTTAGGATGGGTGTGGAATAAGTTTTGATGTGGAATTGCAC  
ATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATAAATTGTGTATCTTCCAG  
CCAGGAATCCTACACGCCAGCATGTATTTCTACAAATAAAGTTTTCTTTGCATACCAAAAAAAA  
AAAAA

## **FIGURE 138**

MRQFPKTSFDISPEMSFSIYSLQVPAVPGLTCWALTAEPGWGQNGATTGATNSHSDSELRPEIF  
SSREAWQFFLLWSPDFRPKMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNG  
FSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKIS  
SLANSFLTIKKDLRLSHAMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEET  
E

Important features of the protein:

Signal peptide:

amino acids 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 192-195, 225-228

N-myristoylation sites.

amino acids 42-47, 46-51, 136-141

## FIGURE 139

CCTGGAGCCGGAAGCGCGGCTGCAGCAGGGCGAGGCTCCAGGTGGGGTCGGTTCCGCATCCAGCC  
 TAGCGTGTCCACGATGCGGCTGGGCTCCGGGACTTTCGCTACCTGTTGCGTAGCGATCGAGGTGC  
 TAGGGATCGCGGTCTTCTTCGGGGATTCTTCCCGGCTCCCGTTCGTTCCCTCTGCCAGAGCGGAA  
 CACGGAGCGGAGCCCCCAGCGCCCCGAACCTCGGCTGGAGCCAGTTCTAACTGGACCACGCTGCC  
 ACCACCTCTCTTCAGTAAAGTTGTATTGTTCTGATAGATGCCTTGAGAGATGATTTTGTGTTG  
 GGTCAAAGGGTGTGAAATTTATGCCCTACACAACCTACCTTGTGGAAAAAGGAGCATCTCACAGT  
 TTTGTGGCTGAAGCAAAGCCACCTACAGTTACTATGCCTCGAATCAAGGCATTGATGACGGGGAG  
 CCTTCTCGGCTTTGTGACGTCATCAGGAACCTCAATTCTCTGCACTGCTGGAAGACAGTGTGA  
 TAAGACAAGCAAAAGCAGCTGGAAAAAGAATAGTCTTTTATGGAGATGAAACCTGGGTAAATTA  
 TTCCCAAAGCATTTTTGTGGAATATGATGGAACAACCTCATTTTTCGTGTGAGATTACACAGAGGT  
 GGATAATAATGTACAGAGGCATTTTGATAAAGTATTAAAAAGAGGAGATTGGGACATATTAATCC  
 TCCACTACCTGGGGCTGGACCACATTGGCCACATTTAGGGGCCAACAGCCCCCTGATTGGGCAG  
 AAGCTGAGCGAGATGGACAGCGTGTGATGAAGATCCACACCTCACTGCAGTCGAAGGAGAGAGA  
 GACGCTTTTACCCAATTTGCTGGTTCTTTGTGGTGACCATGGCATGTCTGAAACAGGAAGTCACG  
 GGGCTCTCTCCACCAGGAGGTGAATACACCTCTGATTTTAAATCAGTTCTGCGTTTGAAAGGAAA  
 CCCGGTGATATCCGACATCCAAAGCAGTCCAAATAGACGGATGTGGCTGCGACACTGGCGATAGC  
 ACTTGGCTTACCGATTCCAAAAGACAGTGTAGGGAGCCTCTATTCCCAGTTGTGGAAGGAAGAC  
 CAATGAGAGAGCAGTTGAGATTTTACATTTGAATACAGTGCAGCTTAGTAAACTGTTGCAAGAG  
 AATGTGCCGTATATGAAAAAGATCCTGGGTTTGAGCAGTTTAAATGTGAGAAAGATTGCATGG  
 GAACTGGATCAGACTGTACTTGGAGGAAAAGCATTGAGAAGTCTATTCAACCTGGGCTCCAAGG  
 TTCTCAGGCAGTACCTGGATGCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCACAAGTGGCCAG  
 TTCTCACCCCTGCTCCTGCTCAGCGTCCCACAGGCACTGCACAGAAAGGCTGAGCTGGAAGTCCCA  
 CTGTCTATCTCCTGGGTTTCTCTGCTCTTTTATTTGGTGATCCTGGTTCCTTTCGGCCGTTACGT  
 CATTTGTGTGACCTCAGCTGAAAGTTTCGTGCTACTTCTGTGGCTCTCGTGGCTGGCGGCAGGCT  
 GCCTTTTCGTTTACCAGACTCTGGTTGAACACCTGGTGTGTGCCAAGTGTGGCAGTGCCTGGAC  
 AGGGGGCTCAGGGAAGGACGTGGAGCAGCCTTATCCAGGCCTCTGGGTGTCCCGACACAGGTG  
 TTCACATCTGTGCTGTCAGGTCAGATGCCTCAGTTCTTGGAAGCTAGGTTCTCTGCGACTGTTAC  
 CAAGGTGATTGTAAAGAGCTGGCGGTACAGAGGAACAAGCCCCCAGCTGAGGGGGTGTGTGAA  
 TCGGACAGCCTCCAGCAGAGGTGTGGGAGCTGCAGCTGAGGGAAGAAGAGACAATCGGCCTGGA  
 CACTCAGGAGGGTCAAAGGAGACTTGGTCGCACCACTCATCTGCCACCCCAAGAAATGCATCCT  
 GCCTCATCAGGTCCAGATTTCTTTCCAAGGCGGACGTTTTCTGTTGGAATTCTTAGTCTTTGGCC  
 TCGGACACCTTCATTCTAGCTGGGGAGTGGTGGTGAGGCAGTGAAGAAGAGGCGGATGGTCAC  
 ACTCAGATCCACAGAGCCAGGATCAAGGGACCCACTGCAGTGGCAGCAGGACTGTTGGGCCCCC  
 ACCCAACCTGACAGCCCTCATCCCTCTTGGCTTGAGCCGTGAGAGCCCTGTGCTGAGTGT  
 CTGACCGAGACACTCACAGCTTTGTATCAGGGCACAGGCTTCCTCGGAGCCAGGATGATCTGTG  
 CCACGCTTGACCTCGGGCCCATCTGGGCTCATGCTCTCTCTCTGCTATTGAATTAGTACCTAG  
 CTGCACACAGTATGTAGTTACCAAAAGAATAAACGGCAATAATTGAGAAAAAAA

## **FIGURE 140**

MRLGSGTFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGAEPPAPEPSAGASSNWTTLPPPLF  
SKVVIVLIDALRDDFVFGSKGVKFMPTTYLVEKGASHSFVAEAKPPTVTMPRIKALMTGSLPGF  
VDVIRNLNSPALLEDSEVIRQAKAAGKRIVFYGDETWVKLFPKHFEYDGTTSFFVSDYTEVDNNV  
TRHLDKVLKRGDWDILILHYLGLDGHISGPN SPLIGQKLSEMDSVLMKIHTSLQSKERETPLP  
NLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKPGDIRHPKHVQ

**Important features of the protein:**

**Signal peptide:**

amino acids 1-34

**Transmembrane domain:**

amino acids 58-76

**N-glycosylation sites.**

amino acids 56-60, 194-198

**N-myristoylation sites.**

amino acids 6-12, 52-58, 100-106, 125-131, 233-239, 270-276,  
275-281, 278-284

**Amidation site.**

amino acids 154-158

**Cell attachment sequence.**

amino acids 205-208

## FIGURE 141

GGCACGAGGCAAGCCTTCCAGGTTATCGTGACGCACCTTGAAAGTCTGAGAGCTACTGCCCTACA  
GAAAGTTACTAGTGCCCTAAAGCTGGCGCTGGCACTGATGTTACTGCTGCTGTTGGAGTACAAC  
TCCCTATAGAAAACAACTGCCAGCACCTTAAGACCACTCACACCTTCAGAGTGAAGAACTTAAAC  
CCGAAGAAATTGAGCATTCATGACCAGGATCACAAAGTACTGGTCCTGGACTCTGGGAATCTCAT  
AGCAGTTCCAGATAAAAACTACATACGCCCCAGAGATCTTCTTTGCATTAGCCTCATCCTTGAGCT  
CAGCCTCTGCGGAGAAAGGAAGTCCGATTCTCCTGGGGGTCTCTAAAGGGGAGTTTGTCTCTAC  
TGTGACAAGGATAAAGGACAAAGTCATCCATCCCTTCAGCTGAAGAAGGAGAAACTGATGAAGCT  
GGCTGCCCCAAAGGAATCAGCACGCCCGGCCCTTCATCTTTTATAGGGCTCAGGTGGGCTCCTGGA  
ACATGCTGGAGTCGGCGGCTCACCCGGATGGTTCATCTGCACCTCCTGCAATTGTAATGAGCCT  
GTTGGGGTGACAGATAAATTTGAGAACAGGAAACACATTGAATTTTCATTTCAACCAGTTTGCAA  
AGCTGAAATGAGCCCCAGTGAGGTCAGCGATTAGGAAACTGCCCCATTGAACGCCTTCCTCGCTA  
ATTTGAACTAATTGTATAAAAAACACCAAACCTGCTCACT

## **FIGURE 142**

MLLLLLEYNFPNIENNCQHLKTTHTFRVKNLNPKKFSIHDQDHKVLVLDSGNLIAVPDKNYIRPEI  
FFALASSLSSASAEKGSPIILLGVSKGEFCLYCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFI  
FYRAQVGSWNMLESAAHPGWFICTSCNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 33-36

N-myristoylation site.

amino acids 50-55, 87-92

Interleukin-1

amino acids 37-182

## FIGURE 143

CTAGAGAGTATAGGGCAGAAGGATGGCAGATGAGTGACTCCACATCCAGAGCTGCCTCCCTTTAA  
TCCAGGATCCTGTCCTTCTGTCTCTGTAGGAGTGCCTGTTGCCAGTGTGGGGTGAGACAAGTTTG  
TCCCACAGGGCTGTCTGAGCAGATAAGATTAAGGGCTGGGTCTGTGCTCAATTAAGTCTGTGGG  
CACGGGGGCTGGGAAGAGCAAAGTCAGCGGTGCCTACAGTCAGCACCATGCTGGGCCTGCCGTGG  
AAGGGAGGTCTGTCTGGGCGCTGCTGCTGCTTCTCTTAGGCTCCCAGATCCTGCTGATCTATGC  
CTGGCATTTCACGAGCAAAGGGACTGTGATGAACACAATGTCATGGCTCGTTACCTCCCTGCCA  
CAGTGGAGTTTGCTGTCCACACATTCAACCAACAGAGCAAGGACTACTATGCCTACAGACTGGGG  
CACATCTTGAATTCCTGGAAGGAGCAGGTGGAGTCCAAGACTGTATTCTCAATGGAGCTACTGCT  
GGGGAGAACTAGGTGTGGGAAATTTGAAGACGACATTGACAACTGCCATTTCCAAGAAAGCACAG  
AGCTGAACAATACTTTACCTGCTTCTTACCATCAGCACCAGGCCCTGGATGACTCAGTTCAGC  
CTCCTGAACAAGACCTGCTTGGAGGGATTCCACTTCAGTGAAACCCACTCACAGGCTTGTCCATGT  
GCTGCTCCACATTCCGTGGACATCAGCACTACTCTCCTGAGGACTCTTCAGTGGCTGAGCAGCT  
TTGGACTTGTGTTTATCCTATTTTGCATGTGTTTGAGATCTCAGATCAGTGTGTTTAGAAAATCC  
ACACATCTTGAGCCTAATCATGTAGTGTAGATCATTAAACATCAGCATTTTAAGAAAAAAAAAA  
AA

## **FIGURE 144**

MLGLPWKGGLSWALLLLLLLGSQILLIYAWHFHEQRDCDEHNVMARYLPATVEFAVHTFNQQSKDY  
YAYRLGHILNSWKEQVESKTVFSMELLGRTRCGKFEDDIDNCHFQESTELNNTFTCFFTISTRP  
WMTQFSLINKTCLEGFH

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**N-glycosylation sites.**

amino acids 117-121, 139-143

**N-myristoylation site.**

amino acids 9-15



## FIGURE 145

CTGTGCAGCTCGAGGCTCCAGAGGCACACTCCAGAGAGAGCCAAGGTTCTGACGCGATGAGGAAG  
CACCTGAGCTGGTGGTGGCTGGCCACTGTCTGCATGCTGCTCTTCAGCCACCTCTCTGCGGTCCA  
GACGAGGGGCATCAAGCACAGAATCAAGTGGAAACCGGAAGGCCCTGCCAGCACTGCCAGATCA  
CTGAGGCCAGGTGGCTGAGAACCGCCCGGGAGCCTTCATCAAGCAAGGCCGCAAGCTCGACATT  
GACTTCGGAGCCGAGGGCAACAGGTACTACGAGGCCAACTACTGGCAGTTCCCCGATGGCATCCA  
CTACAACGGCTGCTCTGAGGCTAATGTGACCAAGGAGGCATTGTGACCGGCTGCATCAATGCCA  
CCCAGGCGGCGAACCAGGGGGAGTTCCAGAAGCCAGACAACAAGCTCCACCAGCAGGTGCTCTGG  
CGGCTGGTCCAGGAGCTCTGCTCCCTCAAGCATTGCGAGTTTGGTTGGAGAGGGGCGCAGGACT  
TCGGGTCACCATGCACCAGCCAGTGCTCCTCTGCCTTCTGGCTTTGATCTGGCTCATGGTGAAAT  
AAGCTTGCCAGGAGGCTGGCAGTACAGAGCGCAGCAGCGAGCAAATCCTGGCAAGTGACCCAGCT  
CTTCTCCCCCAAACCCACGCGTGTCTGAAGGTGCCAGGAGCGGCGATGCACTCGCACTGCAAA  
TGCCGCTCCCACGTATGCGCCCTGGTATGTGCCTGCGTTCTGATAGATGGGGGACTGTGGCTTCT  
CCGTCACTCCATTCTCAGCCCCTAGCAGAGCGTCTGGCACACTAGATTAGTAGTAAATGCTTGAT  
GAGAAGAACACATCAGGCACTGCGCCACCTGCTTCACAGTACTTCCCAACAACCTCTTAGAGGTAG  
GTGTATTCCCGTTTTACAGATAAGGAAACTGAGGCCAGAGAGCTGAAGTACTGCACCCAGCATC  
ACCAGCTAGAAAGTGGCAGAGCCAGGATTCAACCCCTGGCTTGTCTAACCCAGGTTTTCTGCTCT  
GTCCAATTCCAGAGCTGTCTGGTGATCACTTTATGTCTCACAGGGACCCACATCAAACATGTAT  
CTCTAATGAAATTGTGAAAGCTCCATGTTTAGAAATAAATGAAAACACCTGA

## **FIGURE 146**

MRKHLSWWLATVCMLLFSLHSAVQTRGIKHRIKWNRKALPSTAQITEAQVAENRPGAFIKQGRK  
LDIDFGAEGNRYYEANYWQFPDGIHYNGCSEANVTKEAFVTGCINATQAAHQGEFQKPDNKLHQQ  
VLWRLVQELCSLKHCEFWLERGAGLRVTMHQPVLLCLLALIWMVK

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-26

#### **Transmembrane domain:**

amino acids 157-171

#### **N-glycosylation sites.**

amino acids 98-102, 110-114

#### **Tyrosine kinase phosphorylation site.**

amino acids 76-83

#### **N-myristoylation sites.**

amino acids 71-77, 88-94, 93-99, 107-113, 154-160

#### **Amidation site.**

amino acids 62-66

## **FIGURE 147**

GCCTTGGCCTCCCAAAGGGCTGGGATTATAGGCGTGACCACCATGTCTGGTCCAGAGTCTCATTT  
CCTGATGATTTATAGACTCAAAGAAAACTCATGTTTCAGAAGCTCTCTTCTCTTCTGGCCTCCTCT  
CTGTCTTCTTTCCCTCTTTCTTCTTATTTTAATTAGTAGCATCTACTCAGAGTCATGCAAGCTGG  
AAATCTTTCATTTTGCTTGTCAGTGGGGTAGGTCAGTCTTAGTTTTATTTTTTGAAATTT  
CAACTTTCAGATTCAGGGGGTACATGTGAAGGTTTGTTTTATGAGTATATTGCATTGATGCTGAGG  
TTTGGGGT

## **FIGURE 148**

MFRSSLLFWPPLCLLSLFLLLILISSIYSESKLEIFHFACQWGRSLSLSFYFLKFQLSDSGGTCE  
GLFYEYIA

Important features of the protein:

Signal peptide:

amino acids 1-25

N-myristoylation site.

amino acids 62-68

## FIGURE 149

GTCTCCGCGTCACAGGAACCTTCAGCACCCACAGGGCGGACAGCGCTCCCCTCTACCTGGAGACTTGAC  
TCCCGCGCGCCCCAACCCCTGCTTATCCCTTGACCGTCGAGTGTGAGAGATCCTGCAGCCGCCAGTCC  
CGGCCCCCTCTCCCGCCCCACACCCACCCCTCCTGGCTCTTCTGTGTTTTACTCCTCCTTTTCATTGATA  
ACAAAAGCTACAGCTCCAGGAGCCCAGCGCCGGGCTGTGACCCAAGCCGAGCGTGGAAGAATGGGGTT  
CCTCGGGACCGGCACTTGGATTCTGGTGTTAGTGCTCCCGATTCAAGCTTTCCCAAACCTGGAGGAA  
GCCAAGACAAATCTCTACATAATAGAGAATTAAGTGCAGAAAGACCTTTGAATGAACAGATTGCTGAA  
GCAGAGAAGACAAGATTAAAAAACATATCCTCCAGAAAACAAGCCAGGTGAGAGCAACTATTCTTT  
TGTTGATAACTTGAACCTGCTAAAGGCAATAACAGAAAAGGAAAAAATTGAGAAAGAAAGACAATCTA  
TAAGAAGCTCCCCACTTGATAATAAGTTGAATGTGGAAGATGTTGATTCAACCAAGAATCGAAAAGT  
ATCGATGATTATGACTCTACTAAGAGTGGATTGGATCATAAATTTCAAGATGATCCAGATGGTCTTCA  
TCACTAGACGGGACTCCTTTAACCCTGAAGACATTGTCCATAAAATCGCTGCCAGGATTTATGAAG  
AAAATGACAGAGCCGTGTTTGACAAGATTGTTTCTAACTACTTAATCTCGGCCTTATCACAGAAAGC  
CAAGCACATACACTGGAAGATGAAGTAGCAGAGGTTTTACAAAATTAATCTCAAAGGAAGCCAACAA  
TTATGAGGAGGATCCCAATAAGCCCAAGCTGGACTGAGAATCAGGCTGGAAAAATACCAGAGAAAAG  
TGACTCCAATGGCAGCAATTCAAGATGGTCTTGCTAAGGGAGAAAACGATGAAACAGTATCTAACACA  
TTAACCTTGACAAATGGCTTGGAAGGAGAACTAAAACCTACAGTGAAGACAACCTTTGAGGAACCTCCA  
ATATTTCCCAAATTTCTATGCGCTACTGAAAAGTATTGATTGAGAAAAAGCAAAAGAGAAAGAAA  
CACTGATTACTATCATGAAAACACTGATTGACTTTGTGAAGATGATGGTGAAATATGGAACAATATCT  
CCAGAAGAAGGTGTTTCTACCTTGAAAACCTGGATGAAATGATTGCTCTTCAGACCAAAAACAGCT  
AGAAAAAATGCTACTGACAATATAAGCAAGCTTTTCCAGCACCATCAGAGAAGAGTCATGAAGAAA  
CAGACAGTACCAAGGAAGAAGCAGCTAAGATGGAAAAGGAATATGGAAGCTTGAAGGATTCCACAAAA  
GATGATAACTCCAACCCAGGAGGAAAGACAGATGAACCCAAAGGAAAAACAGAAGCCTATTTGGAAGC  
CATCAGAAAAAATATTGAATGGTTGAAGAAACATGACAAAAGGGAAATAAAGAAGATTATGACCTTT  
CAAAGATGAGAGACTTCATCAATAAAACAAGCTGATGCTTATGTGGAGAAAGGCATCCTTGACAAGGAA  
GAAGCCGAGGCCATCAAGCGCATTATAGCAGCCTGTAAAAATGGCAAAAGATCCAGGAGTCTTTCAA  
CTGTTTCAGAAAACATAATATAGCTTAAACACTTCTAATTCTGTGATTAAAAATTTTTGACCCAAGG  
GTTATTAGAAAGTGTGAATTTACAGTAGTTAACCTTTTACAAGTGGTTAAACATAGCTTTCTTCCC  
GTAAAAACTATCTGAAAGTAAAGTTGTATGTAAGCTGAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 150**

MGFLGTGTWILVLVLP IQAFPKPGGSQDKSLHNRELSAERPLNEQIAEAEEDKIKKTYPPENKPG  
QSNYSFVDNLNLLKAITEKEKIEKERQSIRSSPLDNKLNVEDVDSTKNRKLIDDDYSTKSGLDHK  
FQDDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDEVAE  
VLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMAAIQDGLAKGENDETVSNTLTLTNGLE  
RRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKMMVKYGTISPEEGV  
SYLENLDEMIALQTKNLEKNATDNISKLFAPSEKSHEETDSTKEEAAKMEKEYGSLKDSTKDD  
NSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYDL SKMRDFINKQADAYVEKGILDK  
EEAEA IKRIYSSL

### **N-glycosylation sites:**

amino acids 68-71, 346-349, 350-353

### **Casein kinase II phosphorylation site:**

amino acids 70-73, 82-85, 97-100, 125-128, 147-150, 188-191, 217-  
220, 265-268, 289-292, 305-308, 320-323, 326-329, 362-365, 368-  
341, 369-372, 382-385, 386-389, 387-390

### **N-myristoylation sites:**

amino acids 143-148, 239-244

## FIGURE 151

CGGCTCGAGGCTCCCGCCAGGAGAAAGGAACATTCTGAGGGGAGTCTACACCTGTGGAGCTCAA  
**GATG**GTCTCTGAGTGGGGCGCTGTGCTTCCGAATGAAGGACTCGGCATTGAAGGTGCTTTATCTGC  
ATAATAACCAGCTTCTAGCTGGAGGGCTGCATGCAGGGAAGGTCATTAAAGGTGAAGAGATCAGC  
GTGGTCCCAATCGGTGGCTGGATGCCAGCCTGTCCCCCGTCATCCTGGGTGTCCAGGGTGAAG  
CCAGTGCCTGTCTGTGGGGTGGGGCAGGAGCCGACTCTAACACTAGAGCCAGTGAACATCATGG  
AGCTCTATCTTGGTGCCAAAGGAATCCAAGAGCTTCACCTTCTACCGGCGGGACATGGGGCTCACC  
TCCAGCTTCGAGTCCGGTGCCTACCCGGGCTGGTTCCTGTGCACGGTGCCTGAAGCCGATCAGCC  
TGTCAGACTCACCAGCTTCCCGAGAATGGTGGCTGGAATGCCCCATCACAGACTTCTACTTCC  
AGCAGTGTGAC**TAG**GGCAACGTGCCCCCAGAATCCCTGGGCAGAGCCAGCTCGGGTGAGGGGT  
GAGTGGAGGAGACCATGGCGGACAATCACTCTCTGCTCTCAGGACCCACGCTGACTTAG  
TGGGCACCTGACCACTTTGTCTTCTGGTTCCTCCAGTTTGGATAAATTCTGAGATTGGAGCTCAGT  
CCACGGTCTCCCCACTGGATGGTGTCTACTGCTGTGGAACCTTGTAACCATGTGGGGTAA  
CTGGGAATAACATGAAAAGATTTCTGTGGGGGTGGGGTGGGGGAGTGGTGGGAATCATTCCTGCT  
TAATGGTAACTGACAAGTGTACCCCTGAGCCCCGAGGCCAACCATCCCCAGTTGAGCCTTATA  
GGGTCACTAGCTCTCCACATGAAGTCTGTCACTCACCAGTGTGCAGGAGAGGGAGGTGGTCATA  
GAGTCAGGATCTATGGCCCTTGGCCAGCCCCACCCCTTCCCTTTAATCCTGCCACTGTCTATA  
TGCTACCTTTCTATCTCTTCCCTCATCATCTTGTGTGGGCATGAGGAGGTGGTGTATGCAGAA  
GAAATGGCTCGAGCTCAGAAGATAAAAGATAAGTAGGGTATGCTGATCCTCTTTAAAAACCCAA  
GATACAATCAAATCCCAGATGCTGGTCTCTATTCCCATGAAAAAGTGTCTATGACATATTGAGA  
AGACCTACTTACAAAGTGGCATATATGCAATTTATTTTAAATAAAAGATACCTATTTATATATT  
TCTTTATAGAAAAAGTCTGGAAGAGTTTACTTCAATTGTAGCAATGTGAGGGTGGTGGCAGTAT  
AGGTGATTTTTCTTTAATTCTGTTAATTTATCTGTATTTCCCTAATTTTCTACAATGAAGATGA  
ATTCTTTGTATAAAAAAAGAAAAGAAATTAATCTTGAGGTAAGCAGAGCAGACATCATCTCTGA  
TTGTCTCAGCCTCCACTTCCCCAGAGTAAATTCAAATTGAATCGAGCTCTGCTGCTCTGGTTGG  
TTGTAGTAGTGATCAGGAAACAGATCTCAGCAAGCCACTGAGGAGGAGGCTGTGCTGAGTTTGT  
GTGGCTGGAATCTCTGGGTAAGGAACCTTAAAGAACAAAAATCATCTGGTAATTTCTTCTAGAA  
GATCACAGCCCCCTGGGATTCGAAGCATTGGATCCAGTCTCTAAGAAGGCTGCTGTACTGGTTGA  
ATTGTGTCCCCCTCAAATTCACATCCTTCTTGGAACTCAGTCTGTGAGTTTATTTGGAGATAAG  
GTCTCTGCAGATGTAGTTAGTTAAGACAAGGTCATGCTGGATGAAGGTAGACCTAAATTCATAT  
GACTGGTTTCTTGTATGAAAAGGAGAGGACACAGAGACAGAGGAGACGCGGGGAAGACTATGTA  
AAGATGAAGGCAGAGATCGGAGTTTTCAGCCACAAGCTAAGAAACACCAAGGATTGTGGCAACC  
ATCAGAAGCTTGGAAGAGGCAAGAAGAATTCTTCCCTAGAGGCTTTAGAGGGATAACGGCTCTG  
CTGAAACCTTAATCTCAGACTTCCAGCCTCCTGAACGAAGAAAGAATAAATTCGGCTGTTTTAA  
GCCACCAAGGATAATTGGTTACAGCAGCTCTAGGAACTAATACAGCTGCTAAAATGATCCCTGT  
CTCCTCGTGTTTACATTCTGTGTGTGTCCCCCTCCACAATGTACCAAAGTTGTCTTTGTGACCAA  
TAGAATATGGCAGAAGTGATGGCATGCCACTTCCAAGATTAGGTTATAAAAGACACTGCAGCTTC  
TACTTGAGCCCTCTCTCTGCCACCCACCGCCCCAATCTATCTTGGCTCACTCGCTCTGGGGG  
AAGCTAGCTGCCATGCTATGAGCAGGCCTATAAAGAGACTTACGTGGTAAAAAATGAAGTCTCCT  
GCCCACAGCCACATTAGTGAACCTAGAAGCAGAGACTCTGTGAGATAATCGATGTTTGTGTTTT  
AAGTTGCTCAGTTTTTGGTCTAATTGTTATGCAGCAATAGATAAATAATATGCAGAGAAAGAG

## **FIGURE 152**

MVLSGALCFRMKDSALKVLYLHNNQLLAGGLHAGKVIKGEEISVVPNRWLDASLSPVILGVQGS  
QCLSCGVGQEPTLTLEFPVNIMELYLGAKESKSFTFYRRDMGLTSSFESAAYPGWFLCTVPEADQP  
VRLTQLPENGGWNAPITDFYFQQCD

### **N-myristoylation sites.**

amino acids 29-34, 30-35, 60-65, 63-68, 73-78, 91-96, 106-111

### **Interleukin-1 signature.**

amino acids 111-131

### **Interleukin-1 proteins.**

amino acids 8-29, 83-120, 95-134, 64-103



## FIGURE 153

CTTCAGAACAGGTTCTCCTTCCCCAGTCACCAAGTTGCTCGAGTTAGAATTGTCTGCAATGGCCGC  
CCTGCAGAAATCTGTGAGCTCTTTCCTTATGGGGACCCTGGCCACCAGCTGCCTCCTTCTCTTGG  
CCCTCTTGGTACAGGGAGGAGCAGCTGCGCCCATCAGCTCCCACTGCAGGCTTGACAAGTCCAAC  
TTCCAGCAGCCCTATATCACCAACCGCACCTTCATGCTGGCTAAGGAGGCTAGCTTGGCTGATAA  
CAACACAGACGTTCTGCTCATTGGGGAGAACTGTTCCACGGAGTCAGTATGAGTGAGCGCTGCT  
ATCTGATGAAGCAGGTGCTGAACCTTACCCTTGAAGAAGTGTGTTCCCTCAATCTGATAGGTTT  
CAGCCTTATATGCAGGAGGTGGTGCCTTCCCTGGCCAGGCTCAGCAACAGGCTAAGCACATGTCA  
TATTGAAGGTGATGACCTGCATATCCAGAGGAATGTGCAAAAGCTGAAGGACACAGTGAAAAAGC  
TTGGAGAGAGTGGAGAGATCAAAGCAATTGGAGAAGTGGATTGCTGTTTATGTCTCTGAGAAAT  
GCCTGCATTTGACCAGAGCAAAGCTGAAAAATGAATAACTAACCCCTTCCCTGCTAGAAATAA  
CAATTAGATGCCCCAAAGCGATTTTTTTTAAACCAAAGGAAGATGGGAAGCCAACTCCATCATG  
ATGGGTGGATTCCAAATGAACCCCTGCGTTAGTTACAAAGGAAACCAATGCCACTTTTGTATTATA  
AGACCAGAAGGTAGACTTTCTAAGCATAGATATTTATTGATAACATTTTCATTGTAAGTGGTGTTT  
TATACACAGAAAACAATTTATTTTTTAAATAATTGTCTTTTCCATAAAAAAGATTACTTTCCAT  
TCCTTTAGGGGAAAAAACCCCTAAATAGCTTCATGTTTCCATAATCAGTACTTTATATTTATAAA  
TGTATTTATTATTATTATAAGACTGCATTTTATTATATCATTTTATTAATATGGATTATTTAT  
AGAAACATCATTCGATATTGCTACTTGAGTGTAAGGCTAATATTGATATTTATGACAATAATTAT  
AGAGCTATAACATGTTTATTTGACCTCAATAAACACTTGGATATCCC

## **FIGURE 154**

MAALQKSVSSFLMGTLATSCLLLLLVQGGAAAPISSHCRLDKSNFQQPYITNRTFMLAKEASL  
ADNNTDVRLIGEKLFGVSMSERCYLMKQVLNFTLEEVLFPQSDRFQPYMQEVVPFLARLSNRLS  
TCHIEGDDLHIQRNVQKLKDTVKKLGESGEIKAIGELDLLFMSLRNACI

**Important features of the protein:**

**Signal peptide:**

amino acids 1-33

**N-glycosylation sites.**

amino acids 54-58, 68-72, 97-101

**N-myristoylation sites.**

amino acids 14-20, 82-88

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 10-21

## FIGURE 155

GGCTTGCTGAAAATAAAATCAGGACTCCTAACCTGCTCCAGTCAGCCTGCTTCCACGAGGCCCTGT  
CAGTCAGTGCCCCGACTTGTGACTGAGTGTGCAGTGCCAGCATGTACCAGGTCACTGCAGAGGGC  
TGCCCTGAGGGCTGTGCTGAGAGGGAGAGGAGCAGAGATGCTGCTGAGGGTGGAGGGAGGCCAAGC  
TGCCAGGTTTGGGGCTGGGGGCCAAGTGGAGTGAGAACTGGGATCCCAGGGGGAGGGTGCAGAT  
GAGGGAGCGACCCAGATTAGGTGAGGACAGTTCTCTCATTAGCCTTTTCCTACAGGTGGTTGCAT  
TCTTGGCAATGGTCATGGGAACCCACACCTACAGCCACTGGCCCAGCTGCTGCCCCAGCAAAGGG  
CAGGACACCTCTGAGGAGCTGCTGAGGTGGAGCACTGTGCCTGTGCCTCCCCTAGAGCCTGCTAG  
GCCCCAACCGCCACCCAGAGTCCTGTAGGGCCAGTGAAGATGGACCCCTCAACAGCAGGGCCATCT  
CCCCCTGGAGATATGAGTTGGACAGAGACTTGAACCGGCTCCCCAGGACCTGTACCACGCCCCGT  
TGCCCTGTGCCCCGCACTGCGTCAGCCTACAGACAGGCTCCACATGGACCCCGGGGCAACTCGGA  
GCTGCTCTACCACAACCAGACTGTCTTCTACAGGCGGCCATGCCATGGCGAGAAGGGCACCCACA  
AGGGCTACTGCCTGGAGCGCAGGCTGTACCGTGTTCCTTAGCTTGTGTGTGTGTGCGGCCCGGT  
GTGATGGGCTAGCCGGACCTGCTGGAGGCTGGTCCCTTTTGGGAAACCTGGAGCCAGGTGTACA  
ACCACTTGCCATGAAGGGCCAGGATGCCAGATGCTTGCCCCCTGTGAAGTGTCTGTGAGCAG  
CAGGATCCCGGGACAGGATGGGGGGCTTTGGGGAAACCTGCACTTCTGCACATTTTGAAAAGAG  
CAGCTGCTGCTTAGGGCCGCCGAAGCTGGTGTCTCTGTCATTTTCTCTCAGGAAAGGTTTCAAA  
GTTCTGCCCATTTCTGGAGGCCACCACTCCTGTCTCTTCTCTTTTCCCATCCCCTGCTACCCTG  
GCCCAGCACAGGCACTTTCTAGATATTTCCCCCTTGCTGGAGAAGAAAGAGCCCCCTGGTTTTATT  
TGTTTGTTTACTCATCACTCAGTGAGCATCTACTTTGGGTGCATTCTAGTGTAGTTACTAGTCTT  
TTGACATGGATGATTCTGAGGAGGAAGCTGTATTGAATGTATAGAGATTTATCCAAATAAATAT  
CTTTATTTAAAAATGAAAAA

## **FIGURE 156**

MRERPRLGEDSSLISLFLQVVAFLAMVMGTHTYSHWPSCCPSKGQDTSEELLRWSTVPVPPLEPA  
RPNRHPESCRASEDGPLNSRAISPWRYELDRDLNRLPQDLYHARCLCPHCVSLQTGSHMDPRGNS  
ELLYHNQTVFYRRPCHGEKGTHKGYCLERRLYRVSLACVCVRPRVMG

**Important features of the protein:**

**Signal peptide:**

amino acids 1-32

**N-glycosylation site.**

amino acids 136-140

**Tyrosine kinase phosphorylation site.**

amino acids 127-135

**N-myristoylation sites.**

amino acids 44-50, 150-156

## FIGURE 157

CCGGCGATGTCGCTCGCTGCTGCTAAGCCTGGCCGCGCTGTGCAGGAGCGCCGTACCCCGAGAGCC  
GACCGTTCAATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTAATCC  
CCGGAGACTTGAGGGACCTCCGAGTAGAACCTGTTACAACAGTGTGCAACAGGGGACTATTCA  
ATTTTGATGAATGTAAGCTGGGTACTCCGGGCAGATGCCAGCATCCGCTTGTGAAGGCCACCAA  
GATTTGTGTGACGGGCAAAAGCAACTTCCAGTCTACAGCTGTGTGAGGTGCAATTACACAGAGG  
CCTTCCAGACTCAGACCAGACCCTCTGGTGGTAAATGGACATTTTCTACATCGGCTTCCTGTGA  
GAGCTGAACACAGTCTATTTTATTGGGGCCATAATATTCCTAATGCAAATATGAATGAAGATGG  
CCCTTCCATGTCTGTGAATTTACCTCACCAGGCTGCCTAGACCACATAATGAAATATAAAAAA  
AGTGTGTCAAGGCCGGAAGCCTGTGGGATCCGAACATCACTGCTTGTGAAGAAGATGAGGAGACA  
GTAGAAGTGAACCTCACAACCACTCCCTGGGAAACAGATACATGGCTCTTATCCAACACAGCAC  
TATCATCGGGTTTTCTCAGGTGTTTGAGCCACACCAGAAGAAACAAACGCGAGCTTCAGTGGTGA  
TTCCAGTGACTGGGGATAGTGAAGGTGCTACGGTGTCAGCTGACTCCATATTTTCTTACTTGTGGC  
AGCGACTGCATCCGACATAAAGGAACAGTTGTGCTCTGCCCACAAACAGGCGTCCCTTTCCCTCT  
GGATAACAACAAAAGCAAGCCGGGAGGCTGGCTGCCTCTCCTCCTGCTGTCTCTGCTGGTGGCCA  
CATGGGTGCTGGTGGCAGGGATCTATCTAATGTGGAGGCACGAAAGGATCAAGAAGACTTCCTTT  
TCTACCACCACACTACTGCCCCCATTAAGGTTCTTGTGGTTTACCCATCTGAAATATGTTTCCA  
TCACACAATTTGTTACTTCACTGAATTTCTTCAAACCATTCGAGAAGTGAGGTATCCTTGAAA  
AGTGGCAGAAAAGAAAATAGCAGAGATGGGTCCAGTGCAGTGGCTTGCCACTCAAAGAAGGCA  
GCAGACAAAGTCGTCTTCCTTCTTTCCAATGACGTCAACAGTGTGTGCGATGGTACCTGTGGCAA  
GAGCGAGGGCAGTCCCAGTGAGAACTCTCAAGACCTCTTCCCCCTTGCCTTTAACCTTTTCTGCA  
GTGATCTAAGAAGCCAGATTCTCTGCACAAATACGTGGTGGTCTACTTTAGAGAGATTGATACA  
AAAGACGATTACAATGCTCTCAGTGTCTGCCCCAAGTACCACCTCATGAAGGATGCCACTGCTTT  
CTGTGCAGAACTTCTCCATGTCAAGCAGCAGGTGTCAGCAGGAAAAAGATCACAAGCCTGCCACG  
ATGGCTGCTGCTCCTTGTAG

## **FIGURE 158**

MSLVLLSLAALCRSAVPREPTVQCGSETGPSPEWMLQHDLPGLDLRLRVEPVTTSVATGDYSILMNVS  
LRADASIRLLKATKICVTGKSNFQSYSCVRCNYTEAFQTQTRPSGGKWTFSYIGFPVELNTVYFIGAHNIP  
NANMNEDGPSMSVNFTSPGCLDHIMKYKKKCVKAGSLWDPNITACKKNEETVEVNFTTTPLGNYMALIQH  
STIIGFSQVFEPHQKKQTRASVVIPVTGDSEGATVQLTPYFPTCGSDCIRHKGTVVLCPTGVFPPLDNNK  
SKPGGWLPLLLLSLLVATWVLVAGIYLMWRHERIKKTSFSTTTLLPPIKVLVVYPSEICFHHTICYFTEFL  
QNHCRSEVILEKWQKKKIAEMGPVQWLATQKKAADKVVFLLSNDVNSVCDGTGCGKSEGSPSENSQDLFPLA  
FNLFCSDLRSQIHLHKYVVVYFREIDTKDDYNALSVCPKYHLMKDATAFCAELLHVKKQVSAGKRSQACHD  
GCCSL

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-14

#### **Transmembrane domain:**

amino acids 290-309

#### **N-glycosylation sites.**

amino acids 67 - 71, 103 - 107, 156 - 160, 183 - 187, 197 - 201 and 283 - 287

#### **cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 228 - 232 and 319 - 323

#### **Casein kinase II phosphorylation sites.**

amino acids 178 - 182, 402 - 406, 414 - 418 and 453 - 457

#### **N-myristoylation site.**

amino acids 116-122

#### **Amidation site.**

amino acids 488-452

## **FIGURE 159**

AGCCACCAGCGCAACATGACAGTGAAGACCCTGCATGGCCCAGCCATGGTCAAGTACTTGCTGCT  
GTCGATATTGGGGCTTGCCTTTCTGAGTGAGGCGGCAGCTCGGAAAATCCCCAAAGTAGGACATA  
CTTTTTTCCAAAAGCCTGAGAGTTGCCCCGCTGTGCCAGGAGGTAGTATGAAGCTTGACATTGGC  
ATCATCAATGAAAACCAGCGCGTTTCCATGTCACGTAACATCGAGAGCCGCTCCACCTCCCCCTG  
GAATTACACTGTCACTTGGGACCCCAACCGGTACCCCTCGGAAGTTGTACAGGCCCAAGTGTAGGA  
ACTTGGGCTGCATCAATGCTCAAGGAAAGGAAGACATCTCCATGAATCCGTTCCCATCCAGCAA  
GAGACCCTGGTCGTCCGGAGGAAGCACCAAGGCTGCTCTGTTTCTTTCCAGTTGGAGAAGGTGCT  
GGTGAAGTGTGGCTGCACCTGCGTCACCCCTGTCATCCACCATGTGCAGTTAAGAGGTGCATATCC  
ACTCAGCTGAAGAAG

## **FIGURE 160**

MTVKTLHGPAVKYLLLSILGLAFLSEAAARKIPKVGHTFFQKPESCPPVPGGSMKLDIGIINEN  
QRVSMsrNIESRSTSPWNYTWTWDPNRYPSVVQAQCRNLGCINAQGGKEDISMNSVPIQQETLVV  
RRKHQGCsvSFQLEKVLVTVGCTCVTPVIHHVQ

**Signal sequence:**

amino acids 1-30

**N-glycosylation site.**

amino acids 83-87

**N-myristoylation sites.**

amino acids 106-111, 136-141



## FIGURE 161

ACACTGGCCAAACAAAAACGAAAGCACTCCGTGCTGGAAGTAGGAGGAGAGTCAGGACTCCCAGG  
ACAGAGAGTGCACAACTACCCAGCACAGCCCCCTCCGCCCCCTCTGGAGGCTGAAGAGGGATT  
CAGCCCCCTGCCACCCACAGACACGGGCTGACTGGGGTGTCTGCCCCCTTGGGGGGGGCAGCAC  
AGGGCCTCAGGCCTGGGTGCCACCTGGCACCTAGAAGATGCTGTGCCCTGGTTCTTGTCTCCT  
TGGCACTGGGCGCAAGCCAGTGGTCTTTCTCTGGAGAGGCTTGTGGGGCCTCAGGACGCTACC  
CACTGCTCTCCGGGCTCTCCTGCCGCTCTGGGACAGTGACATACTCTGCCTGCCTGGGGACAT  
CGTGCCTGCTCCGGGCCCCGTGCTGGCGCCTACGCACCTGCAGACAGAGCTGGTGCTGAGGTGCC  
AGAAGGAGACCGACTGTGACCTCTGTCTGCGTGTGGCTGTCCACTTGGCCGTGCATGGGCACTGG  
GAAGAGCCTGAAGATGAGGAAAAGTTTGGAGGAGCAGCTGACTCAGGGGTGGAGGAGCCTAGGAA  
TGCCTCTCTCCAGGCCCAAGTCGTGCTCTCCTTCCAGGCCTACCCTACTGCCCGCTGCGTCTCTGC  
TGGAGGTGCAAGTGCCTGCTGCCCTTGTGCAAGTTGGTCACTGTGTGGGCTCTGTGGTATATGAC  
TGCTTCGAGGCTGCCCTAGGGAGTGAGGTACGAATCTGGTCTTATACTCAGCCAGGTACGAGAA  
GGAACCTCAACCACACACAGCAGCTGCCTGCCCTGCCCTGGCTCAACGTGTGACGAGATGGTGACA  
ACGTGCATCTGGTTCTGAATGTCTCTGAGGAGCAGCACTTCGGCCTCTCCCTGTACTGGAATCAG  
GTCCAGGGCCCCCAAAACCCCGTGGCACAAAACCTGACTGGACCGCAGATCATTACCTTGAA  
CCACACAGACCTGGTTCCCTGCCCTCTGTATTAGGTGTGGCTCTGGAACCTGACTCCGTTAGGA  
CGAACATCTGCCCTTTCAGGGAGGACCCCGCGCACACCAGAACCTCTGGCAAGCCCGCCGACTG  
CGACTGCTGACCTGTCAGAGCTGGCTGCTGGACGACCGTGTCTGCTGCCCGCAGAAGCGGCACT  
GTGCTGGCGGGCTCCGGGTGGGGACCCCTGCCAGCACTGGTCCACCGCTTTCTGGGAGAACG  
TCACTGTGGACAAGTTCTCGAGTTCCCATTTGCTGAAAGGCCACCCTAACCTCTGTGTTCAAGTG  
AACAGCTCGGAGAAGCTGCAGCTGCAGGAGTGTCTGTGGGCTGACTCCCTGGGGCCTCTCAAAGA  
CGATGTGCTACTGTTGGAGACACGAGGCCCCAGGACAACAGATCCCTCTGTGCCTTGAACCCA  
GTGGCTGTACTTCACTACCCAGCAAAGCCTCCACGAGGGCAGCTCGCCTTGGAGAGTACTTACTA  
CAAGACCTGCAGTCAGGCCAGTGTCTGCAGCTATGGGACGATGACTTGGGAGCGCTATGGGCCTG  
CCCCATGGACAAATACATCCACAAGCGCTGGGCCCTCGTGTGGCTGGCCTGCCTACTCTTTGCCG  
CTGCGCTTTCCCTCATCCTCCTTCTCAAAAAGGATCACGCGAAAGGGTGGCTGAGGCTCTTGAA  
CAGGACGTCCGCTCGGGGGCGGCCCGAGGGGCGCGCGCTCTGCTCCTTACTCAGCCGATGA  
CTCGGGTTTCGAGCGCTGGTGGGCGCCCTGGCGTCCGGCCCTGTGCCAGCTGCCGCTGCGCGTGG  
CCGTAGACCTGTGGAGCCGTCGTGAACCTGAGCGCGCAGGGGCGCCGTGGCTTTTACCGCGCAG  
CGGCGCCAGACCCTGCAGGAGGGCGGCGTGGTGGTCTTGTCTTCTCTCCGCTGCGGTGGCGCT  
GTGCAGCGAGTGGCTACAGGATGGGGTGTCCGGGCCCGGGGCGCACGGCCCGCACGACGCTTCC  
GCGCCTCGCTCAGCTGCGTGTGCCGACTTCTTGAGGGCGGGGCGCCCGGCAGCTACGTGGGG  
GCCTGCTTCGACAGGCTGTCCACCCGACGCGGTACCCGCCCTTTTCCGCACCGTGGCCGTCTT  
CACACTGCCCTCCCAACTGCCAGACTTCTTGGGGGCCCTGCAGCAGCCTCGCGCCCCGCTTCCG  
GGCGGCTCCAAGAGAGCGGAGCAAGTGTCCCGGGCCCTTCAGCCAGCCCTGGATAGCTACTTC  
CATCCCCCGGGGACTCCCGCGCGGACGCGGGTGGGACCAGGGGCGGGACCTGGGGCGGGGA  
CGGGACTTAAATAAAGGCAGACGCTGTTTTTCTAAAAAA

## **FIGURE 162**

MPVPWFLLSLALGRSPVVLSELRVGPQDATHCSPGLSCRLWDS DILCLPGDIVPAPGPVLAPTHLQTELV  
LRCQKETDCDLCLRVAVHLAVHGHWEPEDEEKFGGAADSGVEEPRNASLQAQVVL SFQAYPTARCVLLEV  
QVPAALVQFGQSVGSSVYDCFEAALGSEVRIWSYTQPRYEKELNHTQQLPALPWLNV SADGDNVHLVLNV  
EEQHFGLSLYWNQVQGPVKPRWHKNLTGPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQ  
LWQAARLRLTLQSWLLDAPCSLPAAEALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQ  
VNSSEKLQEQECLWADSLGPKDDVLLLETRGPQDNRS LCALEPSGCTSLPSKASTRAARLGEYLLQDLQS  
GQCLQLWDDDLGALWACPMCKYIHKRWALVWLACLLFAAALSLILLKKDHAKGWLRLLLKQDVRSGAAARG  
RAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELSAQGPVAVFHAQRRQTLQEGGVVLLFSP  
GAVALCSEWLQDGVSGPGANGPHDAFRASLSCVLPDFLQGRAPGSYVGACFDRL LHPDAVPALFRTVPVFT  
LPSQLPDFLQALQQPRAPRSGRLQERAEQVSRA LQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT

### **Signal sequence:**

amino acids 1-20

### **Transmembrane domain.**

amino acids 453-475

### **N-glycosylation sites.**

amino acids 118-121, 186-189, 198-201, 211-214, 238-241, 248-251,  
334-337, 357-360, 391-394

### **Glycosaminoglycan attachment site.**

amino acids 583-586

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 552-555

### **N-myristoylation sites.**

amino acids 107-112, 152-157, 319-324, 438-443, 516-521, 612-617,  
692-697, 696-701, 700-705

## FIGURE 163

GGGAGGGCTCTGTGCCAGCCCCGATGAGGACGCTGCTGACCATCTTGAAGTGTGGGATCCCTGGCT  
 GCTCAGCCCCCTGAGGACCCCTCGGATCTGCTCCAGCACGTGAAATTCAGTCCAGCAACTTTGA  
 AAACATCCTGACGTGGGACAGCGGGCCAGAGGGCACCCAGACACGGTCTACAGCATCGAGTATA  
 AGACGTACGGAGAGAGGGACTGGGTGGCAAAGAAGGGCTGTGACGGATCACCCGGAAGTCTGTC  
 AACCTGACGGTGGAGACGGGCAACCTCACGGAGCTCTACTATGCCAGGGTCACCGCT  
 GTCAGTGCGGGAGGCGGGTCAGCCACCAAGATGACTGACAGGTTGAGTCTCTGCAGCACACTAC  
 CCTCAAGCCACCTGATGTGACCTGTATCTCCAAAGTGAGATCGATTGAGATGATTGTTTCATCCTA  
 CCCCCACGCCAATCCGTGACGGGATGGCCACCGGCTAACCTTGAAGACATCTTCCATGACCTG  
 TTCTACCACTTAGAGCTCCAGGTCAACCGCACCTACCAAATGCACCTTGGAGGGAAGCAGAGAGA  
 ATATGAGTTCTTCGGCTGACCCCTGACACAGAGTTCTTGGCACCATCATGATTGCGTTCCCA  
 CCTGGGCCAAGGAGAGTGCCCCCTACATGTGCCGAGTGAAGACACTGCCAGACCGACATGGACC  
 TACTCCTTCTCCGGAGCCTTCTGTCTCCATGGGCTTCTCGTGCAGTACTCTGCTACCTGAG  
 CTACAGATATGTACCAAGCCGCTGCACCTCCCAACTCCCTGAACGTCCAGCGAGTCTGACTT  
 TCCAGCCGCTGCGCTTCATCCAGGAGCACGTCTGATCCCTGTCTTTGACCTCAGCGGCCCCAGC  
 AGTCTGGCCAGCCTGTCCAGTACTCCAGATCAGGGTGTCTGGACCCAGGGAGCCCGCAGGAGC  
 TCCACAGCGGCATAGCCTGTCCGAGATCACCTACTTAGGGCAGCCAGACATCTCCATCTCCAGC  
 CCTCCAAACGTGCCACCTCCCCAGATCCTCTCCCACTGTCTATGCCCCAAACGCTGCCCTGAG  
 GTCGGGCCCCCATCTATGCACCTCAGGTGACCCCCGAAGCTCAATTCCCATTTACGCCCCACA  
 GGCCATCTCTAAGGTCCAGCCTTCTCTATGCCCCCAAGCCACTCCGGACAGCTGGCTCCCT  
 CCTATGGGGTATGCTGGAAGGTTCTGGCAAAGACTCCCCCACTGGGACACTTTCTAGTCTTAA  
 CACCTTAGGCCTAAAGGTGAGCTTCAGAAAGAGCCACCAGCTGGAAGCTGCATGTTAGGTGGCCT  
 TTCTCTGCAGGAGGTGACCTCCTTGGCTATGGAGGAATCCCAAGAAGCAAAATCATGTCACAGC  
 CCCTGGGGATTTGCACAGACAGAACATCTGACCCAAATGTGTACACAGTGGGGAGGAAGGGACA  
 CCACAGTACCTAAAGGGCCAGCTCCCCCTCCTCTCCTCAGTCCAGATCGAGGGCCACCCCATGTC  
 CCTCCCTTTGCAACCTCCTTCCGGTCCATGTTCCCCCTCGGACCAAGGTCCAAGTCCCTGGGGCC  
 TGCTGGAGTCCCTTGTGTGTCCCAAGGATGAAGCCAAGAGCCAGCCCTGAGACCTCAGACCTG  
 GAGCAGCCACAGAACTGGATTCTCTTTTCAGAGGCCTGGCCCTGACTGTGAGTGGGAGTCCCTG  
 AGGGGAATGGGAAAGGCTTGGTGCTTCTCCCTGTCCCTACCCAGTGTACATCCTTGGCTGTCA  
 ATCCCATGCCTGCCCATGCCACACACTCTGCGATCTGGCCTCAGACGGGTGCCCTTGAGAGAAGC  
 AGAGGGAGTGGCATGCAGGGCCCTGCCATGGGTGCGCTCCTCACCGGAACAAGCAGCATGATA  
 AGGACTGCAGCGGGGAGCTCTGGGGAGCAGCTTGTGTAGACAAGCGCGTGTCTGCTGAGCCCTG  
 CAAGGCAGAAATGACAGTGAAGGAGGAATGCAGGGAACTCCCGAGGTCCAGAGCCCCACCTC  
 CTAACACCATGGATTCAAAGTGCTCAGGGAATTTGCCTCTCCTTGGCCCATTCCTGGCCAGTTTC  
 ACAATCTAGCTCGACAGAGCATGAGGCCCCCTGCCTCTTCTGTCTATTGTTCAAAGGTGGGAAGAGA  
 GCCTGGAAAAGAACCAGGCCTGGAAAAGAACCAGAAGGAGGCTGGGCAGAACCAAGAACCTGC  
 ACTTCTGCCAAGGCCAGGGCCAGCAGGACGGCAGGACTCTAGGGAGGGGTGTGGCTGCAGTCA  
 TTCCAGCCAGGGCAACTGCCTGACGTTGACGATTTTCAGCTTCATTCTCTGATAGAACAAAGC  
 GAAATGCAGGTCCACAGGGAGGGAGACACACAAGCCTTTCTGCAGGCAGGAGTTTCAGACCT  
 ATCCTGAGAATGGGGTTTGAAAGGAAGGTGAGGGCTGTGGCCCTGGACGGGTACAATAACACAC  
 TGTAAGTGTGACAACTTTGCAAGCTCTGCCTTGGGTTGAGCCATCTGGGCTCAAATTCAGC  
 CTACCACTCACAAGCTGTGTGACTTCAAACAAATGAAATCAGTGCCCGAAGCTCGGTTTCCTC  
 ATCTGTAATGTGGGATCATAACACCTACCTCATGGAGTTGTGGTGAAGATGAAATGAAGTCATG  
 TCTTTAAAGTGCTTAATAGTGCCTGGTACATGGGCAGTGCCCAATAAACGGTAGCTATTTAAAAA  
 AAAAAAA

## **FIGURE 164**

MRTLLTILTVGSLAAHAPEDPSDLLQHVKFQSSNFENILTWDSGPEGTPDTVYSIEYKTYGERDW  
VAKKGCQRITRKSCNLTVETGNLTELYARVTAVSAGGRSATKMTDRFSSIQHTTLKPPDVTCIS  
KVRSIQMIVHPTPTPIRAGDGHRLTLEDIFHDLFYHLELQVNRTYQMHLGGKQREYEFFGLTPDT  
EFLGTIMICVPTWAKESAPYMCRVKTLPDRTWTYSFSGAFLESMGFLVAVLCYLSYRYVTKPPAP  
PNSLNVQRVLTFQPLRFIQEHVLIPVFDLSGPSSLAQPVQYSQIRVSGPREPAGAPQRHSLSEIT  
YLGQPDISILQPSNVPPPQILSPLSYAPNAAPEVGPPSYAPQVTPEAQFPFYAPQAISKVQPSSY  
APQATPDSWPPSYGVCMEGSGKDSPTGTLSSPKHLRPKGQLQKEPPAGSCMLGGLSLQEVTSIAM  
EESQEAKSLHQPLGICTDRTSDPNVLHSGEETPQYLKGQLPLLSSVQIEGHPMSLPLQPPSGPC  
SPSDQGPSPWGLLESIVCPKDEAKSPAPETSDLEQPTELDSLFRGLALTQWES

### **Signal sequence.**

amino acids 1-17

### **Transmembrane domain.**

amino acids 233-250

### **N-glycosylation sites.**

amino acids 80-83, 87-90, 172-175

### **N-myristoylation sites.**

amino acids 11-16, 47-52, 102-107, 531-536, 565-570

## FIGURE 165

TGGCCTACTGGAAAAAAAAAAAAAAAAAAGTCACCCGGGCCCGCGGTGGCCACAACATGG  
CTGCGGCGCCGGGGCTGCTCTTCTGGCTGTTTCGTGCTGGGGGCGCTCTGGTGGGTCCCGGGCCAG  
TCGGATCTCAGCCACGGACGGCGTTTCTCGGACCTCAAAGTGTGCGGGACGAAGAGTGCAGCAT  
GTTAATGTACCGTGGGAAAGCTCTTGAAGACTTCACGGGCCCTGATTGTCGTTTTGTGAATTTTA  
AAAAAGGTGACGATGTATATGTCTACTACAACTGGCAGGGGGATCCCTTGAACTTTGGGCTGGA  
AGTGTGTAACACAGTTTTTGATATTTTCCAAAAGATTTGATCAAGGTACTTCATAAATACACGGA  
AGAAGAGCTACATATTCAGCAGATGAGACAGACTTTGTCTGCTTTGAAGGAGGAAGAGATGATT  
TTAATAGTTATAATGTAGAAGAGCTTTTAGGATCTTTGGAAGTGGAGGACTCTGTACCTGAAGAG  
TCGAAGAAAGCTGAAGAAGTTTCTCAGCACAGAGAGAAATCTCCTGAGGAGTCTCGGGGGCGTGA  
ACTTGACCCTGTGCCTGAGCCCAGGCATTTCAGAGCTGATTTCAGAGGATGGAGAAGGTGCTTTCT  
CAGAGAGCACCGAGGGGCTGCAGGGACAGCCCTCAGCTCAGGAGAGCCACCCTCACACCAGCGGT  
CCTGCGGCTAACGCTCAGGGAGTGCAGTCTTCGTTGGACACTTTTGAAGAAATTCTGCACGATAA  
ATTGAAAGTGCCGGGAAGCGAAAGCAGAACTGGCAATAGTTCTCCTGCCTCGGTGGAGCGGGAGA  
AGACAGATGCTTACAAAGTCCTGAAAACAGAAATGAGTCAGAGAGGAAGTGGACAGTGCCTTATT  
CATTACAGCAAAGGATTTTCGTTGGCATCAAAATCTAAGTTTGTGTTTACAAAGATTGTTTTTAGTA  
CTAAGCTGCCTTGGCAGTTTGCATTTTTGAGCCAAACAAAAATATATTATTTTCCCTTCTAAGTA  
AAAAAAAAAAAAAAAAAAAA

## **FIGURE 166**

MAAAPGLLFWLFLGALWWVPGQSDLSHGRRFSDLKVCGDEECSSMLMYRGKALEDFTGPDCRFVN  
FKKGDDVYVYYKLAGGSLELWAGSVEHSFGYFPKDLIKVLHKYTEELHIPAETDFVCFEGGRD  
DFNSYNVEELLGSLELEDSPVEESKKAEEVSQHREKSPEESRGRELDPVPEPEAFRAEDGEDGA  
FSESTEGLOGQPSAQESHPTSGPAANAQGVQSSLDTFEEILHDKLKVPGSESRTGNSSPASVER  
EKTDAYKVLKTEMSQRGSGQCVIHYSKGFRWHQNLSLFYKDCF

**Important features of the protein:**

**Signal peptide:**

amino acids 1-22

**N-glycosylation site.**

amino acids 294-298

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 30-34

**Tyrosine kinase phosphorylation site.**

amino acids 67-76

**N-myristoylation sites.**

amino acids 205-211, 225-231, 277-283

**Amidation site.**

amino acids 28-32

## FIGURE 167

CCAGGACCAGGGCGCACCGGCTCAGCCTCTCACTTGTCAGAGGCCGGGGAAGAGAAGCAAAGCGC  
AACGGTGTGGTCCAAGCCGGGGCTTCTGCTTCGCTCTAGGACATACACGGGACCCCTAACTTC  
AGTCCCCCAAACGCGCACCTCGAAGTCTTGAATCCAGCCCCGACATCCACGCGGGCACAGG  
CGCGGCAGGCGGCGAGGTCCCGGCCGAAGGCGATGCGGCGAGGGGTCGGGCAGCTGGGCTCGGGC  
GGCGGGAGTAGGGCCCGCAGGGAGGCGAGGCTGCATATTCAGAGTCGCGGGCTGCGCCCTG  
GGCAGAGGCGCCCTCGCTCCACGCAACACCTGCTGCTGCCACCGCGCCGCGCATGAGCCGCTGG  
TCTCGCTGCTGCTGGGCGCGCGTCTGCTGCGGCCACGGAGCCTTCTGCCGCGCGTGGTCAGC  
GGCCAAAAGGTGTGTTTTGCTGACTTCAAGCATCCCTGCTACAAAATGGCCTACTTCCATGAAC  
GTCCAGCCGAGTGAGCTTTCAGGAGGCACGCCTGGCTTGTGAGAGTGAGGGAGGAGTCCCTCTCA  
GCCTTGAGAATGAAGCAGAAGTAAATAGAGAGCATGTTGCAAAACCTGACAAAACCCGGG  
ACAGGGATTTCTGATGGTGATTTCTGGATAGGGCTTTGGAGGAATGGAGATGGGCAACATCTGG  
TGCCTGCCAGATCTCTACCAGTGGTCTGATGGAAGCAATCCAGTACCGAAACTGGTACACAG  
ATGAACCTTCTGCGGAAGTGAAGTGTGTTGTGATGTATCACAACCAACTGCCAATCTGGC  
CTTGGGGTCCCTACCTTTACCAGTGAATGATGACAGGTGAACATGAAGCACAATTATATTTG  
CAAGTATGAACCAGAGATTAATCCAACAGCCCCGTAGAAAAGCCTTATCTTACAAATCAACCAG  
GAGACACCCATCAGAATGTGGTTGTTACTGAAGCAGGTATAATCCCAATCTAATTTATGTTGTT  
ATACCAACAATACCCCTGCTCTTACTGATACTGGTTGCTTTTGAACCTGTTGTTTCCAGATGCT  
GCATAAAAGTAAAGGAAGAACAACAACTAGTCCAAACAGTCTACACTGTGGATTTCAAAGAGTA  
CCAGAAAAGAAAGTGGCATGGAAGTATAATACTCATTGACTTGGTTCCAGAATTTTGAATTTCT  
GGATCTGTATAAGGAATGGCATCAGAACAATAGCTTGAATGGCTTGAATCACAAGGATCTGC  
AAGATGAAGTGTAAAGTCCCTTTCAGGCAATATTAAGTAATTTTTATATGTCTATTATTTCA  
TTTAAAGAATATGCTGTGCTAATAATGGAGTGAGACATGCTTATTTTGCTAAAGGATGCACCCAA  
ACTTCAAACCTCAAGCAAATGAAATGGACAATGCAGATAAAGTGTATCAACACGTCGGGAGTA  
TGTGTGTTAGAAGCAATTCCTTTTATTTCTTTACCTTTTCAAGTTGTTATCTAGTCAATGTAA  
TGTATATTGTATTGAAATTTACAGTGTGCAAAAGTATTTTACCTTTGCATAAGTGTGTTGATAAAA  
ATGAAGTGTCTAATATTTATTTTATGGCATCTCATTTTCAATACATGCTCTTTTGATTAAAG  
AAACTTATTACTGTTGTCAACTGAATTCACACACACACAAATATAGTACCATAGAAAAAGTTGT  
TTTCTCGAAATAATTCATCTTTCAGCTTCTCTGCTTTTGGTCAATGTCTAGGAAATCTCTCAGA  
AATAAGAAGCTATTTCAATTAAGTGTGATATAAACCTCCTCAAACATTTTACTTAGAGGCAAGGAT  
TGCTTAATTTCAATTGTGCAAGACATGTGCCTTATAATTATTTTAGCTTAAATTAACAGATT  
TTGTAATAATGTAACCTTGTAAATAGGTGCATAAAACATAATGCAGTCAATTTGAACAAAAGAAG  
TGACATACACAATATAAATCATATGTCTTCACACGTTGCCTATATAATGAGAAGCAGCTCTCTGA  
GGGTTCTGAAATCAATGTGGTCCCTCTCTTGCCCACTAAACAAAGATGGTTGTTGCGGGTTTGGG  
ATTGACACTGGAGGCAGATAGTTGCAAGTTAGTCTAAGGTTCCCTAGCTGTATTTAGCCTCTG  
ACTATATTAGTATACAAAGAGGTCATGTGGTTGAGACCAGGTGAATAGTCACTATCAGTGTGGAG  
ACAAGCACAGCACACAGACATTTAGGAAGGAAAGGAACACGAAATCGTGTGAAATGGGTTGG  
AACCCTCAGTGATCGCATATTCATTGATGAGGGTTTGCTTGAGATAGAAAATGGTGGCTCCTTT  
CTGTCTTATCTCCTAGTTTCTTCAATGCTTACGCCTTGTTCTTCTCAAGAGAAAGTTGTAACCTCT  
CTGGTCTTCATATGTCCCTGTGCTCCTTTTAAACCAATAAAGAGTTCTTGTCTTGGGGGAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 168**

MSRVVSLLLGAALLCGHGAFCRRVVSQKVCFADEKHPCKMAYFHELSSRVSFQEARLACESE  
GGVLLSLENEAEQKLIESMLQNLTKPGTGISDGDGFWIGLWRNGDGQTSGACPDLYQWSDGSNSQ  
YRNWYTDEPSCGSEKCVVMYHQPTANPGLGGPYLYQWNDDRCNMKHNICKYEPEINPTAPVEK  
PYLTNQPGDTHQNVVTEAGIIPNLIYVVIPTIPLLLLILVAFGTCCFQMLHKSCKGRKTKTSPNQ  
STLWISKSTRKESGMEV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**Transmembrane domain:**

amino acids 214-235

**N-glycosylation sites.**

amino acids 86-89, 255-258

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 266-269

**N-myristoylation sites.**

amino acids 27-32, 66-71, 91-96, 93-98, 102-107, 109-114, 140-145, 212-217